

137 File copy
Non Elected Representatives
Page 1

OM protein - protein search, using sw model
 Run on : April 17, 2001, 15:38:47 ; Search (with
 title: US-09-446-543A-5
 perfect score: 172
 sequence: 1 SRAHQHSMEIRTPDINPAWVAGRGIRPVGVRF
 scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 searched: 374700 seqs, 117207915 residues
 total number of hits satisfying chosen parameters:
 minimum db seq length: 0
 maximum db seq length: 200000000

Ltd.

21	49.5
22	49.5
23	49.5
24	49.5
25	48.5
26	48.5
27	48.5
28	48.5
29	48.5
30	48.5
31	48.5
32	48.5
33	48.5
34	48.5
35	48.5
37	48.5
38	48.5
39	48.5
39	47.5
40	47.5
41	47.5
42	47.5
43	47.5
44	47.5
45	46.5

Post-processing: minimum match 0%
Maximum Match 100%
Listing first 45 summaries

ALIGNMENT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

No.	Score	Match Length	DB ID	Description
1	104	60.5	13	Q9w624 carassius a
2	62	36.0	2	Q9IAU6 rhodospiril
3	61	35.5	428	097859 bos taurus
4	57	33.1	54	Q9UJF9 homo sapien
5	57	33.1	465	060687 homo sapien
6	56	32.6	4	Q9UQ49 homo sapien
7	56	32.6	629	Q9NQE1 homo sapien
8	55	32.0	1236	Q9JP44 rhodococcus
9	54.5	31.7	503	Q9RK11 vibrio chol
10	53.5	31.1	176	Q98689 saccharomy
11	53	30.8	376	Q9RYP2 deinococcus
12	52	30.2	1292	Q9ZGE5 heliobacil
13	51	29.7	294	Q91K30 caenobibdi
14	51	29.7	315	Q87474 burkholderi
15	51	29.7	430	Q97142 methanobact
16	51	29.7	863	Q9VRV3 dirosophila
17	50.5	29.4	790	Q9m371 arabidopsis
18	50	29.1	503	Q9nsc6 arabidopsis
19	50	29.1	5	Q9LSC6 arabiadoppi
				076383 caenorhabdi

21	48.5	28.2	127	5	Q9W2F6	Q9W2F6 drosophila
22	48.5	28.2	232	6	Q9N0A7	Q9N0A7 macaca fasc
23	48.5	28.2	548	10	Q91fa0	arabidopsis
24	48.5	28.2	877	5	Q9NE42	leishmania
25	48	27.9	223	2	Q85605	prevotella
25	48	27.9	314	2	Q06348	mycobacter
27	48	27.9	343	3	Q74569	coprinus cl
28	48	27.9	348	5	Q45431	cænorhabdi
29	48	27.9	365	10	Q8UT53	schizosacch
30	48	27.9	772	10	Q81349	081349 chlamydomon
31	48	27.9	1330	2	Q55284	synechocyst
32	48	27.9	1331	2	P73020	P73020 syncrocyst
33	48	27.9	1379	10	Q07893	07893 antirrhinum
34	48	27.9	1380	10	Q40001	040001 hordeum vul
35	48	27.9	1381	10	Q39049	039049 arabiopsis
36	48	27.9	1382	10	Q22435	022435 nicotiana t
37	48	27.9	1383	10	Q65808	glycine max
38	47.5	27.6	596	2	Q86468	Rhodobacter
39	47	27.3	455	2	Q33340	033340 mycobacteri
40	47	27.3	785	1	Q86276	086276 methanobacte
41	47	27.3	940	2	Q9KUW5	09KUW5 vibrio chol
42	47	27.3	1084	5	Q9TW4	Q9TW4 caenorhabdi
43	47	27.3	1300	11	Q9J9M2	09J9M2 mus musculu
44	47	27.3	1308	11	Q9JM52	09JM52 mus musculu
45	46.5	27.0	196	10	Q9LFL7	Q9LFL7 streptocarp
ALIGNMENTS						
RESULT	1					
99W624	ID	PRELIMINARY;	PRT:	117 AA.		
99W624	ID	Q9W624:				
	AC	09W624;				
	DR	01-NOV-1999 (TREMBLrel. 12; Last sequence update)				
	DT	01-NOV-1999 (TREMBLrel. 12; Last annotation update)				
	DR	C-REF AMIDE PRECURSOR.				
	OS	Carassius auratus (Goldfish).				
	OC	Bukarwaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterigii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Carassius.				
	OC	Actinopterigii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Carassius.				
	OX	NCBI_TAXID=7957;				
	RN	[1]				
	RP	SEQUENCE FROM N.A.				
	RC	TISSUE: BRAIN;				
	RA	Satake H., Minakata H., Fujimoto M.;				
	RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
	DR	EMBL: AB020024; BAA76621; -;				
	SEQUENCE	117 AA; D5DC4C522038CC2B0 CRC64;				
RESULT	2					
Q918J6	ID	Q918J6	PRELIMINARY;	PRT:	692 AA.	
Q918J6	ID	Q918J6				
AC	Q918J6;					
DT	01-OCT-2000 (TREMBLrel. 15; Created)					
DT	01-OCT-2000 (TREMBLrel. 15; Last sequence update)					
DT	01-OCT-2000 (TREMBLrel. 15; Last annotation update)					
DE	BCIH (FRAGMENT).					
GN	BCRH.					
OS	Rhodospirillum rubrum.					

OC	Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;	OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC	Rhodospirillum;	OC	NCBI_TAXID=9606;
OX	NCBI_TAXID=1085;	OX	
RN	[1]	RN	
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=R5;	RC	Lawlor S.:
RX	MEDLINE=20138142; Pubmed=10671438;	RX	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RA	Cheng Y., Bantner C.A., Tspin A., Collins M.L.P.;	RA	DR EMBL; AL035608; CAB55682.1; -.
RT	"Role of the H protein in assembly of the photochemical reaction	RT	NON_TER 54 54
RT	center and intracytoplasmic membrane in Rhodospirillum rubrum.";	RT	SEQUENCE 54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;
RL	J. Bacteriol. 182:1200-1207 (2000).	RL	
DR	EMBL; AF202319; ARF31352.1; -.	DR	
PT	NON_TER 1	PT	
SQ	SEQUENCE 692 AA; 75453 MW; 96430AE93BF35680 CRC64;	SQ	
Query Match	36.0%; score 62; DB 2; Length 692;	Query Match	33.1%; Score 57; DB 4; Length 54;
Best Local Similarity	40.6%; Pred. No. 0.96;	Best Local Similarity	56.2%; Pred. No. 0.34;
Matches	13; Conservative 4; Mismatches 9; Indels 6; Gaps 1;	Matches	9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY	3 AHQHSMEIRPDINPAWAG----RGIRPV 28	QY	12 TPDPINPAWAGRGIRP 27
Db	568 AEQVSLETRRALPKWKGMLAHGVEGYRQI 599	Db	18 TRAVTPWYAGSGYYP 33
RESULT	3	RESULT	5
ID	097859 PRELIMINARY; PRT; 428 AA.	ID	060687 PRELIMINARY; PRT; 465 AA.
AC	097859; DT 01-MAY-1999 (TREMBLrel. 10, created)	AC	060687; DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-MAY-1999 (TREMBLrel. 10, last sequence update)	DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	GANGLIOSIDE STALIDASE.	DE	SUSHI-REPEAT PROTEIN.
OS	BOS taurus (Bovine).	OS	Homo sapiens (Human).
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Bovidae; Bovinae; Bos.	OC	Mammalia; Eutheria; Primates; Catarhini; Homidae; Homo.
OX	NCBI_TAXID=9913;	OX	NCBI_TAXID=9606;
RN	[1]	RN	
SEQUENCE FROM N.A.		SEQUENCE FROM N.A.	
RC	TISSUE=BRAIN;	RC	
RX	MEDLINE=99143165; Pubmed=9988745;	RX	
RA	Miyagi T., Wada T., Iwamatsu A., Hata K., Yoshioka Y., Tokuyama S.,	RA	Kurokawa H., Inui T., Inaba T., Goi K., Chang K.-S., Sinyo T.,
RA	Sawada M.;	RA	Rakestraw K.M., Naeve C.W., Look T.A.;
RT	"Molecular cloning and characterization of a plasma membrane-	RT	Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RT	associated sialidase specific for gangliosides.";	DR	DR EMBL; AF060567; AAC15765.1; -.
RL	J. Biol. Chem. 274:5004-5011 (1999).	DR	INTERPRO; IPR004436; -.
DR	EMBL; AB008184; BAM75071.1; -.	DR	INTERPRO; IPR001128; -.
DR	INTERPRO; IPRO02060; -.	DR	PFAM; PF00084; Sushi_3.
DR	PFAM; PF02012; BNR; 3.	DR	PROSITE; PS00085; CYTOCHROME_P450; UNKNOWN_I.
SQ	SEQUENCE 428 AA; 47916 MW; 418B34F3245A8F21 CRC64;	SQ	SEQUENCE 465 AA; 52971 MW; 4D732B187FF3EFB8 CRC64;
Query Match	35.5%; Score 61; DB 6; Length 428;	Query Match	33.1%; Score 57; DB 4; Length 465;
Best Local Similarity	40.7%; Pred. No. 0.8;	Best Local Similarity	56.2%; Pred. No. 3.3;
Matches	11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;	Matches	9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY	2 RAHQHSMEIRPDINPAWAGRGIRPV 28	QY	12 TPDPINPAWAGRGIRP 27
Db	195 RARPHSLMISYDDLGATWNGRGLKPM 221	Db	18 TRAVTPWYAGSGYYP 33
RESULT	4	RESULT	6
Q9UJF9	PRELIMINARY; PRT; 54 AA.	Q9UQ49	PRELIMINARY; PRT; 428 AA.
ID	Q9UJF9	ID	Q9UQ49;
AC	Q9UJF9; DT 01-MAY-2000 (TREMBLrel. 13, Created)	AC	Q9UQ49; DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)	DT	01-MAY-2000 (TREMBLrel. 14, last annotation update)
DT	01-JUN-2000 (TREMBLrel. 14, last annotation update)	DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	DJ479J7.3 (SUSHI REPEAT PROTEIN (SRP1)) (FRAGMENT).	DE	GANGLIOSIDE STALIDASE.
GN	Homo sapiens (Human).	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS	Fatigante, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Mammalia; Eutheria; Primates; Catarhini; Homidae; Homo.
OC		OC	NCBI_TAXID=9606;
RT		RT	[1]
SEQUENCE FROM N.A.		SEQUENCE FROM N.A.	
TISSUE=BRAIN;		TISSUE=BRAIN;	
RA	Wada T., Yoshioka Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T.,	RA	"Cloning, expression, and chromosomal mapping of a human ganglioside
RT		RT	sialidase."

RL	Biochem. Biophys. Res. Commun.	261:21-27(1999).
EMBL	AB008185; BARB2611.1;	- .
INTERPRO	IPR028860; -.	
PFAM	PF02012; BNR; 3.	
SEQUENCE	428 AA;	48252 MW;
SO	35D1DD9359A7BC9B CRC64;	J. Biol. Chem. 269:2477-2484(1994).
Db	195 KIRPHSLMIVSDDLGVTHHGRLIRPM 221	[3]
RESULT	7	Query Match 32.6%; Score 56; DB 4; Length 428; Best Local Similarity 37.0%; Pred. No. 4.2; Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
O9NQEL	PRELIMINARY; PRT; 629 AA.	RN SEQUENCE FROM N.A.
ID	O9NQEL	RP STRAIN=ILL44;
AC	O9NQEL;	RC RA
DT	01-OCT-2000 (TREMBLrel. 15, Created)	RT Igarashi N.; shimada K., Matsuura K.V.;
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	RT n PHOTOSYNTHETIC GENE CLUSTER IN PURPLE BACTERIUM, RUBRIVIVAX
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	RT GELATTINOSUS;"
DE	RUBRIVIVAX (EC 3.2.1.18).	RL (in) Garab G. (eds.);
OS	Homo sapiens (Human).	RL Photosynthetic Mechanisms and Effects IV:2889-2892;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RL Kluwer Academic Publishing (1998).
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	RN [4]
OX	NCBI_TaxID=9606;	RN SEQUENCE FROM N.A.
RN	[1] SEQUENCE FROM N.A.	RP STRAIN=ILL44;
RP	SEQUENCE FROM N.A.	RA Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.,
RA	Monti E., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerando B.,	RA Parot P., Vermaglio A.;
RA	Croci G., Pretti A., Ballabio A., Tettamanti G.; Borsani G.;	RT Dark aerobic growth conditions induce the synthesis of a high
RT	*Identification and expression of NEU3, a novel human sialidase associated to the plasma membrane.;"	RT midpoint potential cytochrome c8 in the photosynthetic bacterium
RL	Blochem J. 349:343-351 (2000).	RT Rubrivivax gelatinosus";
DR	EMBL; Y1B563; CAB86131.1; -.	RL Biochemistry 0:0-0(1999).
DR	HYDROLASE; Glycosidase.	DR EMBL; AB034704; BAA94057.1; -.
SQ	SEQUENCE 629 AA; 69702 MW; 97C5464B70B69B4B CRC64;	KW TRANSFERASE 1236 AA; 134729 MW; 84051C045638520C CRC64;
RESULT	8	Query Match 32.6%; Score 56; DB 4; Length 629; Best Local Similarity 37.0%; Pred. No. 6.4; Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
O9JPA4	PRELIMINARY; PRT; 1236 AA.	RN SEQUENCE FROM N.A.
ID	O9JPA4	RP STRAIN=EL TOR NT0961 / SEROTYPE O1;
AC	O9JPA4;	RC MEDLINE=20405833; Published=10952301;
DT	01-OCT-2000 (TREMBLrel. 15, Created)	RA Heidelberg J.F./ Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
DE	MG PROTOPORPHYRIN METHYL TRANSFERASE.	RA Ermolaeva M.D., Vaithianathan J., Bass S., Qin H., Dragoi I., Seilers P.,
GN	BCHH.	RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
OS	Rhodococcus gelatinosus (Rhodopseudomonas gelatinosa).	RA Salzberg S.E., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
OC	Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;	RA Fraser C.M.;
OC	Rubrivirus.	RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
OX	NCBI_TaxID=28068;	RT cholerae.";
RN	[1] SEQUENCE FROM N.A.	RT Nature 406:477-483(2000).
RP	SEQUENCE FROM N.A.	DR EMBL; AB004228; AAF94657.1; -.
RC	STRAIN=ILL44;	DR TIGR; VCI502; - .
RN	Nagashima K.V., Shimada K.; Matsura K.;	SQ SEQUENCE 503 AA; 55597 MW; 2ABD94A2356C9E48 CRC64;
RT	*Phylogenetic analysis of photosynthetic genes of Rhodococcus gelatinosus: possibility of horizontal gene transfer in purple bacteria.";	Query Match 31.7%; Score 54.5; DB 2; Length 503; Best Local Similarity 36.7%; Pred. No. 8.2; Matches 11; Conservative 6; Mismatches 12; Indels 1; Gaps 1
RT	Photosyn. Res. 36:185-191(1993).	RN SEQUENCE FROM N.A.
RN	[2] STRAIN=ILL44;	RC

Tue Apr 17 15:46:14 2001

us-09-446-543a-5.rspt

GenCore version 4.5
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Om protein - protein search, using sw model

Run on : April 17, 2001, 15:39:52 ; Search time 39.1 Seconds
(without alignments)
27.159 Million cell updates/sec

Title: DS-09-446-5.43a-5

perfect score:

Sequence: 1 SRAHQHSMIEKTPDINPAWVAGRGIRPVGKF 31

Scoring table:

Gapp 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	98	I PRRP_BOVIN	P81264 bos taurus
2	163	94.8	83	I PRRP RAT	P81278 rattus norvegicus
3	158	91.9	87	I PRRP_HUMAN	P81277 homo sapien
4	51	29.7	798	I UVRA_METH	P18395 rattus norvegicus
5	51	29.7	962	I UVRA_METH	O26543 methanobacter
6	50	29.1	973	I UVRA_RNTME	P56899 rhizobium m
7	48.5	28.2	239	I 6PGL_SYN3	P74618 synochocystis
8	48.5	28.2	1882	I Y468_MYCIN	P75109 mycoplasma
9	48	27.9	424	I SAMB_SALTY	P28332 salmonella
10	48	27.9	420	I UVRA_TREPA	O83527 treponema p
11	47.5	27.6	1083	I T2D5_HUMAN	O00268 homo sapien
12	47	27.3	406	I DH21_RABBIT	P51976 oryctoideaurs
13	47	27.3	972	I UVRA_MICHAE	P94972 mycobacteri
14	46.5	27.0	770	I AVPL_LARATH	P31414 arabidopsis
15	46	26.7	342	I Y762_METU	O58172 methanococcus
16	46	26.7	347	I 57996_METU	057996 methanococcus
17	46	26.7	510	I YCGB_ECOLI	P29013 escherichia
18	46	26.7	798	I UNR_HUMAN	O75534 homo sapien
19	46	26.7	835	I TGK1_RABBIT	P22758 oryctoideaurs
20	46	26.7	943	I UVRA_HAEIN	P44110 haemophilus
21	45.5	26.5	272	I TRA2_DROVI	O02008 arachnophila
22	45.5	26.5	374	I YPKJ_ECOLI	P31993 escherichia
23	45.5	26.5	411	I PUR1_ARATH	P38025 arabidopsis
24	45.5	26.5	704	I LIP1_NEIMB	O05013 neisseria m
25	45.5	26.2	676	I EXLI_HUMAN	Q22935 homo sapien
26	45	26.2	817	I TGLK_NUMAN	P22735 homo sapien
27	45	26.2	824	I R167_YEAST	P23602 rattus norvegicus
28	45	26.2	940	I UVRA_ECOLI	P07671 escherichia
29	45	26.2	941	I UVRA_SALTY	P37434 salmonella
30	45	26.2	953	I UVRA_RICPR	O93ccc1 rickettsia
31	45	26.2	1033	I ACAC_ABATH	Q91Y7 arabidopsis
32	45	25.2	152	I GST3_HUMAN	O14880 homo sapien
33	44.5	25.9	98	AA: SEQUENCE	10544 MW: 08AC35A13B0FA908 CRC64;

ALIGNMENTS

RESULT 1	PRP_BOVIN	STANDARD:	PRP; 98 AA.
ID PRP_BOVIN			
PRP_BOVIN			
PR	P81264;		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DI	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	PROLACTIN-RELEASING PEPTIDE PRRP (PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASEING PEPTIDE PRRP20).		
DE	RELEASEING PEPTIDE PRRP20).		
GN	PRH-		
OS	Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
OC			
OX			
RN	[1]		
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.		
RC	TISSUE=Brain;		
RX	MEDLINE=88268781; PubMed=9607765;		
RA	Hiduma S.; Habata Y.; Fujii R.; Kawamata Y.; Hosoya M.; Fukusumi S., -Kitada C.; Masuo Y.; Asano T.; Matsumoto H.; Sekiguchi M., Kurokawa T.; Nishimura O.; Onda H.; Fujino M.;		
RA	"A prolactin-releasing peptide in the brain.";		
RL	Nature 393:272-276(1998).		
CC	-I- FUNCTION: STIMULATES PROLACTIN (PRP) RELEASE AND REGULATES THE EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.		
CC	-I- TISSUE SPECIFICITY: MEDULLA OBlongata AND HIPPOTHALAMUS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is In no way modified and this statement is not removed. Usage by and for commercial entities requires a licence agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	DR EMBL: AB015417; BAA29025.1; -		
KW	Hormone; Amidation; Signal; cleavage on pair of basic residues.		
FT	SIGNAL 1		
FT	PROLACTIN-RELEASING PEPTIDE PRRP31.		
FT	PROLACTIN-RELEASING PEPTIDE PRRP20.		
FT	AMIDATION (G-5A PROVIDE AMIDE GROUP).		
FT	MOD_RES 53		
FT	SEQUENCE 98 AA: 10544 MW: 08AC35A13B0FA908 CRC64;		

Query Match	100.0%	Score 172; DB 1;	Length 98;
Best Local Similarity	100.0%	Pred. No. 2.5e-18;	
Matches	31;	Conservative 0; Mismatches 0;	Indels 0; Gaps 0;
OY	1	SRAHQHSMIEKTPDINPAWVAGRGIRPVGKF 31	
Db	23	SRAHQHSMIEKTPDINPAWVAGRGIRPVGKF 53	

RESULT 2

PRP_RAT	STANDARD:	PRT:	83 AA.
ID PRRP_RAT			
AC P81278;			
DT 30-MAY-2000 (Rel. 39, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			
DT 30-MAY-2000 (Rel. 39, Last annotation update)			
DE PROLACTIN-RELEASING PEPTIDE PRRP20) (PROLACTIN-RELEASING HORMONE) (CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20).			
DE PRH.			
GN Rattus norvegicus (Rat).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.			
OC NCBI_TaxID=10116;			
RN {1}			
RP SEQUENCE FROM N.A.			
RC TISSUE=Brain;			

RX MEDLINE=98268781; PubMed=9607765;

RA Hiunma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.,

RA "A prolatin-releasing peptide in the brain.",

RL Nature 393:272-276(1998).

CC -1- FUNCTION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.

CC -1- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.

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CC CC DR EMBL; AB015419; BAA29027.1; -.

CC DR Hormone; Amidation; Signal.

CC FT SIGNAL I 22 BY SIMILARITY.

CC FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP31.

CC FT PEPTIDE 34 53 PROLACTIN-RELEASING PEPTIDE PRRP20.

CC MOD_RES 53 53 AMIDATION (G-53 PROVIDE AMIDE GROUP).

CC SQ SEQUENCE 87 AA; 9639 MW; DDC75A264EE4F29 CRC64;

CC CC DR EMBL; AB015418; BAA29026.1; -.

CC KW Hormone; Amidation; Signal; Cleavage on pair of basic residues.

CC FT SIGNAL 1 21 BY SIMILARITY.

CC FT PEPTIDE 22 52 PROLACTIN-RELEASING PEPTIDE PRRP31.

CC FT PEPTIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRRP20.

CC MOD_RES 52 52 AMIDATION (G-53 PROVIDE AMIDE GROUP).

CC SQ SEQUENCE 83 AA; 9215 MW; DDC75A264EE4F29 CRC64;

CC DR EMBL; AB015418; BAA29026.1; -.

CC KW Hormone; Amidation; Signal; Cleavage on pair of basic residues.

CC FT SIGNAL 1 21 BY SIMILARITY.

CC FT PEPTIDE 22 52 PROLACTIN-RELEASING PEPTIDE PRRP31.

CC FT PEPTIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRRP20.

CC MOD_RES 52 52 AMIDATION (G-53 PROVIDE AMIDE GROUP).

CC SQ SEQUENCE 83 AA; 9215 MW; DDC75A264EE4F29 CRC64;

Query Match 94.8%; Score 163; DB 1; Length 83;

Best local Similarity 93.5%; Pred. No. 4.3e-17;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GT 1 SRABQHSMETRPDPDIPAWYGRGIRPVGRF 31

OY 1 SRABQHSMETRPDPDIPAWYGRGIRPVGRF 31

Db 22 SRABQHSMETRPDPDIPAWYGRGIRPVGRF 52

RESULT 3

PRP_HUMAN	STANDARD:	PRT:	87 AA.
ID PRRP_HUMAN			
AC P81277;			
DT 30-MAY-2000 (Rel. 39, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			
DT 30-MAY-2000 (Rel. 39, Last annotation update)			
DE PROLACTIN-RELEASING PEPTIDE PRRP20) (PROLACTIN-RELEASING HORMONE) (CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20).			
DE PRH.			
GN Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
OC NCBI_TaxID=9605;			
RN {1}			
RP SEQUENCE FROM N.A.			
RC TISSUE=Testis;			

RX MEDLINE=96370473; PubMed=204029;

RA Jeffers M., Paciucci R., Pellicer A.;

RA "Characterization of unr, a gene closely linked to R-ras.",

RL Nucleic Acids Res. 18:4391-4399(1990).

CC -1- FUNCTION: RNA-BINDING PROTEIN (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.

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CC DR EMBL; X52311; CAA6549_1; -.

CC DR PIR; S1210; S1210.

DR HSSP; P15277; IMUC.

DR InterPro; IPR002059; -.
 DR Pfam; PF00313; CSD; 8.
 DR PROSITE; PS00352; COLD_SHOCK; 4.
 KW RNA-binding; Repeat;
 FT DOMAIN 26 87 CSD 1.
 FT DOMAIN 136 179 CSD 2. (INCOMPLETE).
 FT DOMAIN 186 245 CSD 3.
 FT DOMAIN 297 337 CSD 4. (INCOMPLETE).
 FT DOMAIN 349 410 CSD 5.
 FT DOMAIN 447 507 CSD 6.
 FT DOMAIN 519 579 CSD 7.
 FT DOMAIN 610 670 CSD 8.
 SQ SEQUENCE 798 AA; 88894 MW; F484B3FA8B0995A4 CRC64;

Query Match 29.7%; Score 51; DB 1; Length 798;
 Best Local Similarity 43.5%; Pred. No. 9.2;
 Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 6 HSMEITRPDPINPAWPAWRGRPV 28
 Db 583 HSYNGTTEANPTISGKVIRPL 605

RESULT 5
 UVRA_METTH STANDARD PRT; 962 AA.
 AC 026543;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE EXCINUCLEASE ABC SUBUNIT A.
 GN UVRA OR M4H43.
 OS Methanobacterium thermoautotrophicum.
 OC archaea; Euryarchaeia; Methanobacteriales; Methanobacteriaceae;
 OC Methanothermobacter.
 OC NCBI_TAXID=145262;
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DELTAH;
 RX MEDLINE=9371514; PubMed=9371513;
 RA Smith D.R., Doucette-Stamm L.A., Delcourgey C., Lee H.-M., DuBois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keegle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicar R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougal S., Shumer G., Goyal A., Pietrovský S., Church G.M.,
 RA Daniels C.J., Mao J.-T., Rice P., Nolling J., Reeve J.N.,
 RT complete genome sequence of Methanobacterium thermoautotrophicum
 RT functional analysis and comparative genomics.;
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -i FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
 CC CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
 CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE
 CC AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-
 CC STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
 CC -i SUBUNIT: CONSISTS OF THREE SUBUNITS: UVRA, UVRB AND UVRC.
 CC -i SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 CC (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

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 CC or send an email to license@isb-sib.ch);

CC EMBL; AF000838; AAB84949.1; -.
 DR InterPro; IPR001677; -.
 DR Pfam; PF00005; ABC_tran; 2.

DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 KW SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat;
 KW DNA-binding; Zinc-finger.
 FT NP_BIND 38 45 ATP (POTENTIAL).
 FT NP_BIND 649 656 ATP (POTENTIAL).
 FT ZNFING 748 774 CA-TYPE.
 SQ SEQUENCE 962 AA; 108395 MW; 2C05F7FC41CD060 CRC64;

Query Match 29.7%; Score 51; DB 1; Length 962;
 Best Local Similarity 39.5%; Pred. No. 11; 0; Mismatches 5; Indels 18; Gaps 2;
 Matches 15; Conservative 0; Mismatches 15; Indels 18; Gaps 2;
 QY 11 RTPDIDINPAWAG-----RGIRPVGRF 31.
 Db 703 RTFRSNPAPTYGVTHIRELAQTPARKRGVRP-GRF 739

RESULT 6
 UVRA_RHIME STANDARD PRT; 973 AA.
 AC PS0899;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE EXCINUCLEASE ABC SUBUNIT A.
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RA Galibert F., Capera D., Hublet-Barloy F., Gatius M., Batut J.,
 RA Boistard F., Gouzy J., Kahn D., Thebaud P., Goffeau A.,
 RA Puruelle B., Pohl T., Bothé G., Schneider S., Portetelle D.,
 RA Vandendol M., Puehler A., Becker A., Weidner S.;
 RL Submitted (MAY-2000) to the SWISS-PROT data bank.
 RN [2]
 RP SEQUENCE OF 1-140 FROM N.A.
 RC STRAIN=2021;
 RX MEDLINE=99430868; PubMed=10503543;
 RA Tapia A., Barbe J.;
 RT *Regulation of divergent transcription from the uvra-ssb promoters in
 RT Sinorhizobium meliloti.;
 RL Mol. Gen. Genet. 262:121-130 (1999).
 CC -i FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
 CC CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
 CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE
 CC AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-
 CC STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
 CC -i SUBUNIT: CONSISTS OF THREE SUBUNITS: UVRA, UVRB AND UVRC.
 CC -i SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 CC (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

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CC EMBL; AF125162; AAC03210.1; -.
 DR InterPro; IPR001677; -.
 DR PROSITE; PS00211; ABC_TRANSPORTER; PARTIAL.
 KW SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat;
 KW DNA-binding; Zinc-finger.
 FT NP_BIND 34 41 ATP (POTENTIAL).
 FT NP_BIND 662 669 ATP (POTENTIAL).
 CC ZNFING 761 787 CA-TYPE.

Query Match 29.1%; Score 50; DB 1; Length 973;
Best Local Similarity 39.5%; Pred. No. 16;
Matches 15; Conservative 2; Mismatches 3; Indels 18; Gaps 3;

RESULT 7
6PGL SYN3 STANDARD; PRT; 239 AA.
AC P74618; DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 6-PHOSPHOCOLICOLACTONASE (EC 3.1.1.31) (6PGL).
GN PGL OR DEWB OR SLLQ-1479.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TAXID=1148;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=97061201; PUBMED=8905231;
RA Miyajima N., Hirosewa M., Sugihara M., Sasamoto S., Nakamura Y.,
RA Hosouchi T., Matsuno A., Murakai A., Nakazaki N., Naruo K.,
RA Okumura S., Shimojo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RT DNA Res. 3:109-136(1996).
RL [2]
RN [1]
RP SEQUENCE OF 1-19;
MEDLINE=97443574; PUBMED=9298645;
RA Suzuki T., Ohara O.;
RT "Towards a proteome project of cyanobacterium Synechocystis sp.
strain PCC6803: linking 130 protein spots with their respective
genes.;"
RL Electrophoresis 18:1252-1259(1997).
CC "-!- FUNCTION: HYDROLYSIS OF 6-PHOSPHOCOLICOLACTONE TO 6-
CC PHOSPHOGUCONATE."
CC "-!- CATALYTIC ACTIVITY: 6-PHOSPHO-D-GUCONO-1,5-LACTONE + H₂O = 6-
CC PHOSPHO-D-GLUCONATE."
CC "-!- PATHWAY: SECOND STEP IN PENNOSE PHOSPHATE PATHWAY."
CC "-!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
ISOMERASE FAMILY. 6-PHOSPHOCOLICOLACTONE SURFACE."
CC
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RESULT 8
Y468 MYCPN STANDARD; PRT; 1882 AA.
AC P75109; Q50317; DT 01-NOV-1997 (Rel. 35, Created)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN MG468 HOMOLOG (K05_ORF1882).
GN MG684 OR MG158.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TAXID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 29342 / M129;
RA Hilbert H., Himmelreich R., Hilpert H., Plagens H., Pirkle E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
pneumoniae";
RL Nucleic Acids Res. 24:628-639(1996).
RN [2]
RX STRAIN=ATCC 29342 / M129;
RA MEDLINE=6177563; PUBMED=8604303;
RA Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
RT "Sequence analysis of 56 kb from the genome of the bacterium
Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a
cluster of ribosomal protein genes.";
RL Nucleic Acids Res. 24:628-639(1996).
DNA "-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC "-!- SIMILARITY: SOME, TO MG064."
CC
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DR EMBL; AE000117; AA95806.1; -
DR EMBL; U34916; AAC43650.1; -
KW Hypothetical Protein; Transmembrane.
FT TRANSMEM 16 36 POTENTIAL.
FT TRANSMEM 987 1007 POTENTIAL.
FT TRANSMEM 1037 1057 POTENTIAL.
FT TRANSMEM 1080 1100 POTENTIAL.
FT TRANSMEM 1154 1174 POTENTIAL.
FT TRANSMEM 1759 1779 POTENTIAL.
FT TRANSMEM 1807 1827 POTENTIAL.
FT TRANSMEM 1828 1848 POTENTIAL.
FT TRANSMEM 1851 1871 POTENTIAL.
SEQUENCE 1882 AA; 209442 MW; 03CF44D99A7120BD CRC64;

Query Match 28.2%; Score 48.5; DB 1; Length 1882;
Best Local Similarity 32.3%; Pred. No. 52;
Matches 10; Conservative 6; Mismatches 12; Indels 3; Gaps 1;

Query Match 28.2%; Score 48.5; DB 1; Length 239;
Best Local Similarity 42.3%; Pred. No. 6.1;
Matches 11; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

RESULT 9

SAMB_SALTY STANDARD; PRT: 424 AA.

1D SAMB_SALTY *Complete genome sequence of *Treponema pallidum*, the syphilis
AC P23832; RT spirochete; ";
DT 01-NOV-1991 (Rel. 20, last sequence update)
DT 01-NOV-1991 (Rel. 20, last annotation update)
DT 15-DEC-1998 (Rel. 37, last annotation update)

DE SAMB PROTEIN.
GN SAMB.
OS *Salmonella typhimurium*.
OG Plasmid 60-MDa cryptic.
OC *Bacteria*; *Proteobacteria*; gamma subdivision; *Enterobacteriaceae*; *Salmonellales*; *Salmonella*.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LTC2;
RX MEDLINE-9123176; PubMed=1991707;
RA Nohmi T., Hakura A., Nakai Y., Watanabe M., Murayama S.Y., Sofuni T.; *Salmonella typhimurium* has two homologous but different umuDC operons: cloning of a new umuDC-like operon (*samb*) present in a 60-negadation cryptic plasmid of *S. typhimurium*.";
RL J. Bacteriol. 173:1051-1063(1991).
CC !- FUNCTION: INVOLVED IN UV PROTECTION AND MUTATION.
CC !- SIMILARITY: BELONGS TO THE IMPB/MTCB/SAMB FAMILY.
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CC !- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.
CC DR InterPro; IPR00617; -.
CC DR Pfam; PF00005; ABC_tran; 2.
CC DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
CC KW SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat; DNA-binding; Zinc-finger.
FT NP_BIND 35 42 ATP (POTENTIAL).
FT NP_BIND 657 664 C4-TYPE.
FT ZN_FING 270 297 C4-TYPE.
FT ZN_FING 756 782 C4-TYPE.
SQ SEQUENCE 960 AA; 106010 MW; 32E78624B19F7ABF CRC64;
DR EMBL; D90502; BAA14226.1; -.
DR PIR; B38176; B38116.
DR InterPro; IPR001126; -.
DR Pfam; PF00817; IMS_1.
KW Plasmid; SOS mutagenesis; DNA repair.
SQ SEQUENCE 424 AA; 47727 MW; FF8C47476CC58A2B CRC64;

Query Match .27.9%; Score 48; DB 1; Length 424; Best Local Similarity 50.0%; Pred. No. 13; Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY IO RPPDINPAWAGGIRP 27
Db 381 INHPGKGKINFAARGIAP 398

RESULT 10

UVRA_TREPA STANDARD; PRT: 960 AA.

ID UVRA_TREPA 083227; DT 15-DEC-1998 (Rel. 37, created)
ID UVRA_TREPA 15-DEC-1998 (Rel. 37, Last sequence update)
ID UVRA_TREPA 30-MAY-2000 (Rel. 39, Last annotation update)
DE EXCINUCLEASE ABC SUBUNIT A.
GN UVRA_QR TPP054.
QS Treponema pallidum.
OC Spirochaetales; Spirochaetaceae; Treponema.
OC NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRA1=NCIGBOS;
RN MEDLINE-98332770; PubMed=9605876;
RN Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RN Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RN Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RN Khalaila H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RN McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RN Hatch B., Horst K., Roberts R., Sandusky M., Weidman J., Smith H.O.,

RESULT 11

T2D3_HUMAN STANDARD; PRT: 1083 AA.

ID T2D3_HUMAN 000268; Q99721; DT 15-JUL-1998 (Rel. 36, Created)
ID T2D3_HUMAN 15-JUL-1998 (Rel. 36, Last sequence update)
ID T2D3_HUMAN 01-OCT-2000 (Rel. 40, Last annotation update)
DE TRANSCRIPTION INITIATION FACTOR TFIID i35 KDA SUBUNIT (TAIFI1-135) DE (TAIFI135) (TAIFI130) (TAIFI130).
GN TAFC1 OR TAFC2 OR TAIFI135 OR TAIFI130.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97336072; PubMed=912867;
RA Mengus G., May M., Carre I., Chamblon P., Davidson I.;
RT "Human TAF11(i135) potentiates transcriptional activation by the AF-2s of the retinoic acid, vitamin D3, and thyroid hormone receptors in RT mammalian cells.";
RN Genes Dev. 11:1381-1395(1997).
RN [2]
RP SEQUENCE OF 105-1083 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE-97098412; PubMed=8942882;
RA Tanese N., Saluja D., Vassallo M.F., Chen J.-L., Admon A.;
RA "Molecular cloning and analysis of two subunits of the human TFIID complex: hTAIFI130 and hTAIFI100.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:13611-13616(1996).
 CC -!- FUNCTION: MAKES PART OF TFIID IS A MULTIMERIC PROTEIN COMPLEX THAT
 CC PLAYS A CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS
 CC ACTIVATORS AND REPRESSORS. POTENTIATES TRANSCRIPTIONAL ACTIVATION
 CC BY THE AF-2S OF THE RETINOIC ACID, VITAMIN D3 AND THYROID HORMONE.
 CC -!- SUBUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A
 CC NUMBER OF TBP-ASSOCIATED FACTORS (TAFs).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- SIMILARITY: BELONGS TO THE TAF2 FAMILY.

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CC DR EMBL; Y11354; CRA72189.1; --.
 CC DR EMBL; 075308; AAC50301.1; --.
 CC DR HSSP; P19556; 1AFH.
 CC DR MIM; 601796; --.
 KW TRANSCRIPTION REGULATION; NUCLEAR PROTEIN.
 FT DOMAIN 39 42 POLY-HIS.
 FT DOMAIN 52 57 POLY-ALA.
 FT DOMAIN 98 101 POLY-GLY.
 FT DOMAIN 142 148 POLY-ALA.
 FT DOMAIN 268 275 POLY-PRO.
 FT DOMAIN 331 337 POLY-ALA.
 FT DOMAIN 680 683 POLY-PRO.
 FT DOMAIN 808 813 POLY-ALA.
 FT DOMAIN 828 831 POLY-ASP.
 FT CONFLICT 105 117 PGPPSRPRPVPA -> GROLLQORGGRES
 FT CONFLICT 233 264 (IN REF. 2).
 FT CONFLICT 293 293 MISSING (IN REF. 2).
 SQ SEQUENCE 1083 AA; 108943 MW; A6453827572A0752 CRC64;

CC DR U23835; AAA86387.1; --.
 CC DR HSSP; P24061; 1FDV.
 CC DR InterPro; IPR002198; --.
 CC DR Pfam; PF00106; gdh_short; 1.
 CC DR PROSITE; PS00061; ADN_SNR01; 1.
 KW OXIDOREDUCTASE; NAD; MICROSOME.
 FT NP_BIND 82 111 NAD (BY SIMILARITY).
 FT ACT_SITE 232 232 BY SIMILARITY.
 SQ SEQUENCE 406 RA; 44181 MW; F14579663918425D CRC64;

CC DR U23835; AAA86387.1; --.
 CC DR HSSP; P24061; 1FDV.
 CC DR InterPro; IPR002198; --.
 CC DR Pfam; PF00106; gdh_short; 1.
 CC DR PROSITE; PS00061; ADN_SNR01; 1.
 KW OXIDOREDUCTASE; NAD; MICROSOME.
 FT NP_BIND 82 111 NAD (BY SIMILARITY).
 FT ACT_SITE 232 232 BY SIMILARITY.
 SQ SEQUENCE 406 RA; 44181 MW; F14579663918425D CRC64;

RESULT 12
 DH12_RABBIT STANDARD; PRT; 406 AA.
 ID DH12_RABBIT
 AC P51976;
 DT 01-OCT-1995 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CORTICOESTEROID 11-BETA-DHYDROGENASE, ISOMYE 2 (EC 1.1.1.146) (11-
 DE DH2) (11-BETA-NIDROXYSTEROID DEHYDROGENASE 2) (11-BETA-HSD2) (NAD-
 DE DEPENDENT 11-BETA-NIDROXYSTEROID DENHYDROGENASE).
 GN NSD1B2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N37RV;
 RX MEDLINE=98205987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Telkia P.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Horisby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rovers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.J.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.",
 RT Nature 393:537-544(1998).

CC -!- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
 CC CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
 CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN APAPSE
 CC AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-
 CC STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
 CC -!- SUBUNIT: CONSISTS OF THREE SUBUNITS: UVRA, UVRB AND UVRC.

CC THE LEVEL OF THE MINERALOCORTICOID RECEPTOR AND THE GLUCOCORTICOID
 CC -!- FUNCTION: NRAS A ROLE IN MODULATING GLUCOCORTICOID ACTIVITY BOTH AT

CC .-I. SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 CC (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

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DR EMBL; 285982; CAB06633.1; .

DR Tubercolist; RW1638; .

DR InterPro; IPR01617; .

DR Pfam; PF0005; ABC_tran; 2.

DR PROSITE; PS00211; ABC_TRANSPORTER; 2.

KW DNA-response; Excision nuclease; DNA repair; ATP-binding; Repeat;

KW DNA-binding; Zinc-finger.

FT NP_BIND 32 39 . ATP (POTENTIAL).

FT NE_BIND 654 661 ATP (POTENTIAL).

FT FN_FING 257 285 C4-TYPE (ATYPICAL).

FT ZN_FING 753 779 C4-TYPE.

SQ SEQUENCE 972 AA: 106131 MW: 8937A764E592D981 CRC64;

Query Match 27.3%: Score: 47; DB 1; Length 972;

Best Local Similarity 36.8%; Pred. Ho: 43; Mismatches 1; Indexes 18; Gaps 2;

Matches 14; Conservative 1; MisMatches 5; Indexes 18; Gaps 2;

OY 11 RUPDINDAWAG-----RGTRPVGKF 31

Db 708 RPRSPHPATIVGFDKRTIFAMPTERRVRYQP-GRP 744

RESULT 14

ID AVP3_ARATH STANDARD; PRT; 770 AA.

AC P31414; 041919; DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (EC 3.6.1.1) (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE).

GN AVP³.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX HBCL_TAXID=3702;

RH [1]

RH SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=CV_COLUMBIA;

RX MEDLINE-92179255; PubMed-1311852;

RX Sarahan V., Kim Y., Poole R.J., Rea P.A.;" Molecular cloning and sequence of cDNA encoding the pyrophosphate-energized vacuolar membrane proton pump of *Arabidopsis thaliana*."; Proc. Natl. Acad. Sci. U.S.A. 89:1775-1779(1992).

RP SEQUENCE OF 554-671 FROM H.A.

RA STRAIN=CV_COLUMBIA; TISSUE=Green siliques;

RA Raynal M., Greillet F., Laudie M., Meyer Y., Cooke R., Delseny M.; Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.

RH [2]

RH SEQUENCE OF 554-671 FROM H.A.

RA Raynal M., Greillet F., Laudie M., Meyer Y., Cooke R., Delseny M.; Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: CONTRIBUTES TO THE TRANSPORTER (FROM CYTOSOL TO VACUOLE LUMEN) H⁺-ELECTROCHEMICAL POTENTIAL DIFFERENCE. THE H⁺-PPASE ESTABLISHES A H⁺ GRADIENT OF SIMILAR AND OFTEN GREATER MAGNITUDE THAN THE H⁺-ATPASE ON THE SAME MEMBRANE.

-I- CATALYTIC ACTIVITY: PYROPHOSPHATE + H₂O = 2 ORTHOPHOSPHATE.

-I- SUBUNIT: MONOMER.

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. VACUOLAR (TONOPLAST).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/)
CC	or send an email to license@isb-sib.ch .
CC	-----
DR	EMBL: Z17694; CAJ32754.1; -.
DR	PIR: A38230; A38230.
KW	Hydrogen ion transport; Hydrolase; transmembrane; Magnesium.
FT	DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 14 34 INTRAVACUOLAR (POTENTIAL).
FT	TRANSMEM 35 100 POTENTIAL.
FT	TRANSMEM 101 121 INTRAVACUOLAR (POTENTIAL).
FT	DOMAIN 122 142 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 143 163 POTENTIAL.
FT	DOMAIN 154 195 INTRAVACUOLAR (POTENTIAL).
FT	TRANSMEM 196 216 POTENTIAL.
FT	DOMAIN 217 327 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 328 348 POTENTIAL.
FT	DOMAIN 349 368 INTRAVACUOLAR (POTENTIAL).
FT	TRANSMEM 369 389 POTENTIAL.
FT	DOMAIN 390 405 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 406 426 POTENTIAL.
FT	DOMAIN 427 484 INTRAVACUOLAR (POTENTIAL).
FT	TRANSMEM 485 505 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 506 526 POTENTIAL.
FT	TRANSMEM 543 563 INTRAVACUOLAR (POTENTIAL).
FT	DOMAIN 564 573 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 574 594 POTENTIAL.
FT	DOMAIN 595 645 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 645 666 POTENTIAL.
FT	DOMAIN 667 687 INTRAVACUOLAR (POTENTIAL).
FT	TRANSMEM 668 688 POTENTIAL.
FT	DOMAIN 689 746 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 747 767 POTENTIAL.
FT	DOMAIN 768 770 INTRAVACUOLAR (POTENTIAL).
FT	CONFLICT 575 576 T -> A (IN REF. 2).
FT	CONFFLICT 584 584 L -> P (IN REF. 2).
SEQUENCE	770 AA; 80819 MW; CE1132B4B2B299860 CRC64;
RESULT 15	Query Match, Best Local Similarity 27.0%; score 46.5; DB 1; Length 770; Matchers 10; Conservative 9; Mismatches 10; Indels 9; Gaps 1;
QY	1 SRATHOMSERPTPDI-----NPAPWAGRGIRPVG 29
Db	565 SRAGHTIVDYLTPKVLIGLIVGAMPWYNSAMTHNSVY 602
Y762_META	STANDARD: PRT: 342 AA.
ID Y762_META	
AC 058172;	
DT 01-NOV-1997	(Rel. 35, Created)
DT 01-NOV-1997	(Rel. 35, Last sequence update)
DT 01-NOV-1997	(Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN M0762.	
GN MJ0152.	
OS Methanococcus jannaschii.	
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;	
OC Methanococcus.	
OX NCBI_TAXID=2190;	
RN [1]	
RP SEQUENCE FROM N.D.	
RC STRAIN=AL-1	/ DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;	
RA Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Douglar B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkpatrick D., Weinstock J.K., Merrick J.M., Glodkiewicz H., Scott J.L., Geoghegan N.S.M., Weinert K.F., Fuhrmann J.T., Nouman N.,	

RA Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.,
 RA Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Raine, B.P.; Borodovsky, M.,
 RA Klenk, H.-P.; Fraser, C.M.; Smith, H.O.; Weese, C.R.; Venter, J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 Jannaschii";
 RL Science 273:1058-1073 (1996);
 CC "- INTRACELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)."
 CC "- SIMILARITY: STRONG; TO M.JANNASCHII MJ0576 AND TO S.POMBE MALATE
 CC PERMEASE (MAB1).
 CC
 CC

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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

DR EML: U67521; AAB98753; 1; -.
 DR IIGR: MJ0762; -.
 KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; Transport.
 FT TRANSMEM 8 POTENTIAL.
 FT TRANSMEM 39 59 POTENTIAL.
 FT TRANSMEM 79 99 POTENTIAL.
 FT TRANSMEM 108 128 POTENTIAL.
 FT TRANSMEM 142 162 POTENTIAL.
 FT TRANSMEM 175 195 POTENTIAL.
 FT TRANSMEM 207 227 POTENTIAL.
 FT TRANSMEM 242 262 POTENTIAL.
 FT TRANSMEM 276 296 POTENTIAL.
 FT TRANSMEM 304 324 POTENTIAL.
 SQ SEQUENCE 342 AA; 39534 MN; 08EFC3E2C4955D8 CRC64;

Query Match 26.7%; Score 46; DB 1; Length 342;
 Best Local Similarity 43.5%; Pred. No. 21;
 Matches 10; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY	7 SMERTIPDPINPAPWAGRGRPVG	29
Db	: :	149
131 SESIKLDHVNPGRV---IPPGVG		

Search completed: April 17, 2001, 15:48:45
 Job time: 533 sec

QY 1 SRAHQHSMERIIPDINPAWYAGRGRGPVGRF 31
 ||||| ||||| ||||| ||||| |||||
 Db 1 SRAHQHSMERIIPDINPAWYAGRGRGPVGRF 31

RESULT 2 US-09-105-678A-31
 Sequence 31; Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: 48666-342
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REFERENCE/DOCKET NUMBER: 27,026
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

RESULT 3 US-09-105-678A-31
 Query Match 100.0%; Score 172; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 6. 9e-20;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SRAHQHSMERIIPDINPAWYAGRGRGPVGRF 31
 ||||| ||||| ||||| ||||| |||||
 Db 1 SRAHQHSMERIIPDINPAWYAGRGRGPVGRF 31

RESULT 3 US-09-105-678A-32
 Sequence 32; Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.

REGISTRATION NUMBER: 27_026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-6440

TELEFAX: 617-523-6440

SEQUENCE FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

; US-09-105-678A-33

Query Match 100.0%; Score 172; DB 3; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.2e-20;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Db 1 SRAHQHSMETRTPDINPAWYAGRGIRPVGRF 31

RESULT 5

US-09-105-678A-8

Sequence 8, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Sueenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DINE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

ZIP/CITY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: -US/09/105,678A

FILING DATE: 24-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27_026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Db 1 SRAHQHSMETRTPDINPAWYAGRGIRPVGRF 31

RESULT 6

US-09-105-678A-37

Sequence 37, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Sueenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DINE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

ZIP/CITY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: -US/09/105,678A

FILING DATE: 24-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27_026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

SEQUENCE FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

; US-09-105-678A-37

Query Match 94.8%; Score 163; DB 3; Length 31;

Best Local Similarity 93.5%; Pred. No. 1.6e-18;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Db 1 SRAHQHSMETRTPDINPAWYAGRGIRPVGRF 31

RESULT 7

US-09-172-353-4

Sequence 4, Application US/09172353

Patent No. 6197530

GENERAL INFORMATION:

APPLICANT: Stricker-Kongra, Alain

APPLICANT: Gu, Wei

TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS

CURRENT APPLICATION NUMBER: US/09/172,353

CURRENT FILING DATE: 1998-10-14

NUMBER OF SEQ ID NOS: 7

Query Match 94.8%; Score 163; DB 3; Length 31;

Best Local Similarity 93.5%; Pred. No. 1.6e-18;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Db 1 SRAHQHSMETRTPDINPAWYAGRGIRPVGRF 31

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-172-353-4

Query Match Similarity 94.8%; Score 163; DB 3; Length 31;
Best Local Similarity 93.5%; Pred. No. 1.6e-18; Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 SRAHQHSMETRTPDINPAWYAGRGRPVGRF 31
Qy 1 SRAHQHSMETRTPDINPAWYAGRGRPVGRF 31
Db 1 SRAHQHSMETRTPDINPAWYAGRGRPVGRF 31

RESULT 8
US-09-105-678A-38
; Sequence 38, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Sueenga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,678A
; FILING DATE: 26-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 48466-342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; FAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-09-105-678A-39

Query Match Similarity 94.8%; Score 163; DB 3; Length 33;
Best Local Similarity 93.5%; Pred. No. 1.7e-18; Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 SRAHQHSMETRTPDINPAWYAGRGRPVGRF 31
Qy 1 SRAHQHSMETRTPDINPAWYAGRGRPVGRF 31
Db 1 SRAHQHSMETRTPDINPAWYAGRGRPVGRF 31

RESULT 10
US-09-105-678A-29
; Sequence 29, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Sueenga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTY: USA
; ZIP: 02109

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-29

SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-29

Query Match 93.5%; Score 161; DB 3; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3e-18;
 Mismatches 0; Indels 0; Gaps 0;
 Matches 29; Conservative 0;
 Nucleotide Type: peptide

Qy 1 SRAHQHSMEIRTPDINPAWYAGRCIRPVGF 29
 Db 1 SRAHQHSMEIRTPDINPAWYAGRCIRPVGF 29

RESULT 11

US-09-105-678A-9

; Sequence 9, application US/09105678A

; Patent No. 6103882

; GENERAL INFORMATION:

; APPLICANT: Sueenaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26 JUN 1998

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-105-678A-43

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 Best Local Similarity 90.3%; Pred. No. 9.2e-18;
 Mismatches 1; Indels 2; Gaps 0;

; Sequence 43, application US/09105678A

; Patent No. 6103882

; GENERAL INFORMATION:

; APPLICANT: Sueenaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

NEUTRON TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 27-JUN-1997

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

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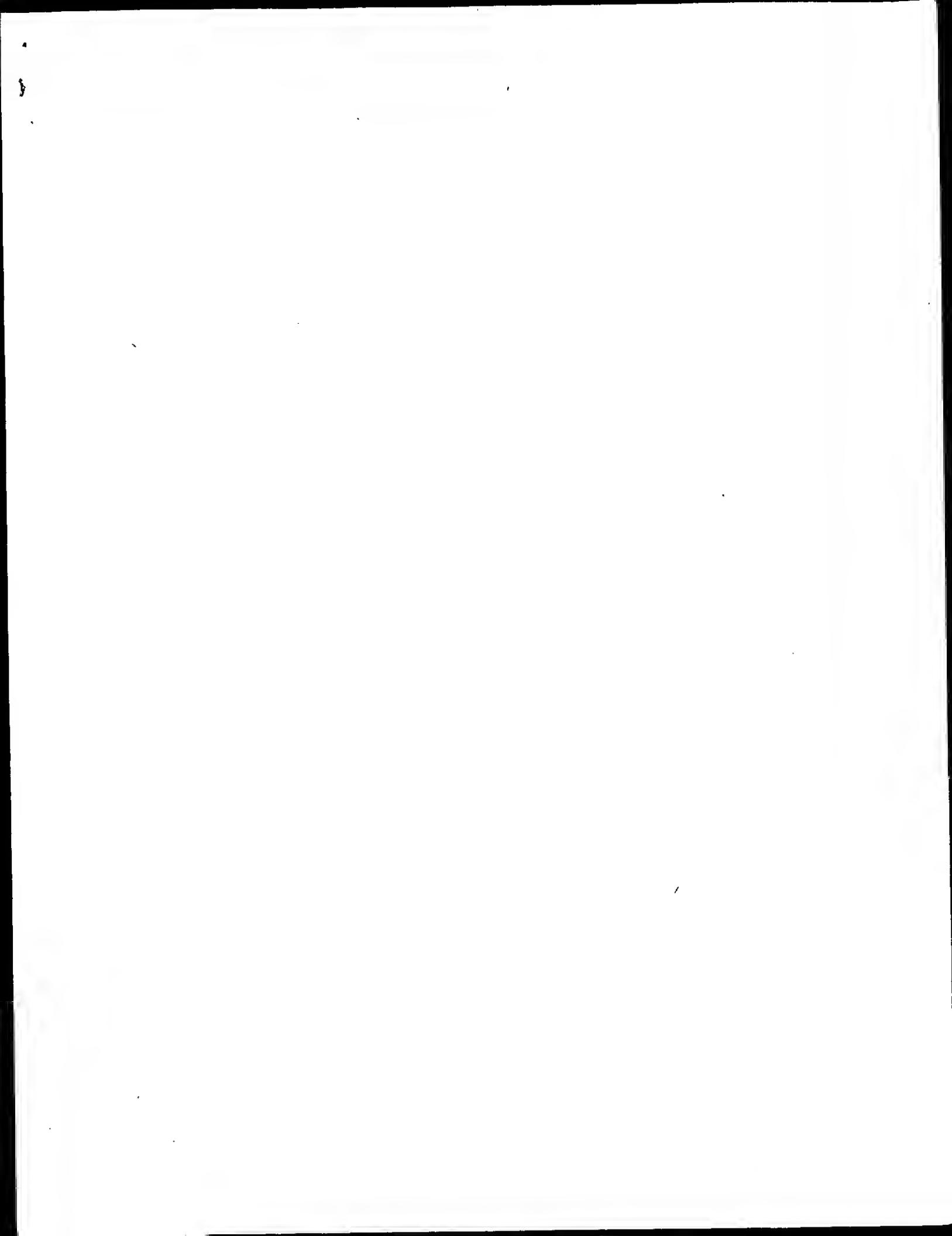
RESULT 13
 US-09-105-678A-44
 ; Sequence 44, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ; APPLICANT: Suenaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
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 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ; US-09-105-678A-45
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 Query Match 91.9%; Score 158; DB 3; Length 32;
 Best Local Similarity 90.3%; Pred. No. 9.6e-18;
 Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 ; US-09-105-678A-44
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 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ; US-09-105-678A-45
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 Best Local Similarity 90.3%; Pred. No. 1e-17;
 Matches 28; Conservative 1; Mismatches 1; Indels 2; Gaps 0;
 Qy 1 SRRAHHSMEIRTPDPINPAWYAGRGIRPVGRF 31
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 Db 1 SRTTHRHSMEIRTPDPINPAWYASRGIRPVGRF 31
 ; US-09-105-678A-44
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-00-105-678A-34

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Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Job time: 316 sec

Db I TPDINPAWYAGRIGIRPVGRF 20



GenCore version 4.5
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OM protein - protein search, using SW model

Run on: April 17, 2001, 15:32:53 ; Search time 116.94 Seconds
 (without alignments)
 15.154 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 172
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	172	100.0	31 20 W87218	Bovine pituitary-d
3	172	100.0	31 20 W87613	Bovine 19P2 ligand
4	172	100.0	31 20 W85188	Bovine pituitary-d
5	172	100.0	31 21 B10347	Bovine oxytocin se
6	172	100.0	31 21 19P2 ligand peptid	19P2 ligand peptid
7	172	100.0	31 21 Y49298	Bovine G protein-c
8	172	100.0	32 18 W31372	Bovine pituitary-d
9	172	100.0	32 20 W95189	Bovine oxytocin se
10	172	100.0	32 21 B10348	Bovine G protein-c
11	172	100.0	33 18 W31373	
SUMMARIES				
RESULT 1				
ID W31371	ID W31371	standard; Peptide: 31 AA.		
XX	XX			
AC W31371;				
DT 06-APR-1998 (first entry)				
DE Bovine G protein-coupled receptor ligand peptide fragment 1.				
XX				
XX				G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.
XX				
OS Bos taurus.				
XX				
PN W09724436-A2.				
PD 10-JUL-1997.				
XX				
PF 26-DEC-1996; 96MO-JP03821.				
XX				
PR 18-SEP-1996; 96JP-0246573.				
PR 28-DEC-1995; 95JP-0343371.				
PR 15-MAR-1996; 95JP-0059419.				
PR 12-AUG-1996; 96JP-0211805.				
XX				
(TAKE) TAKEDA CHEM IND LTD.				
XX				
PI Fuji R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;				
PK Kawama T, Kitada C;				
XX				
WPI: 1997-363672/33.				
DR N-PDB; W02394.				

XX
PT Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland

XX
PT Claim 2; Page 160, 258pp; English.

XX
CC This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 23 to 53 of the sequence in W31368 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hypercholesterolaemia, hyperglycaemia, hyperlipidaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, rheumatoid arthritis, spinal injury, transient brain ischaemia, amyotrophic lateral sclerosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility and/or oligoalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.

XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 172; DB 18; Length 31,
Best local Similarity 100.0%; Pred. No. 3.9e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRANOHSMERITPDPINPAWYAGRGRIPVGRF 31
Db 1 strabghsmeirtpdpinpaawgrrgripvrf 31

RESULT 2
W97218

ID W97218 standard; peptide; 31 AA.
XX
AC
XX
DT 06-MAY-1999 (first entry)

DE Bovine pituitary-derived ligand polypeptide fragment.
XX
KW Bovine pituitary-derived ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypoparathyroidism; gonadotropin secretion; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomata; brain tumour; emmenopothy; autoimmune disease; acromegaly; Chiari-Frommel Syndrome; Argonz-del Castillo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome or dysospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irrigation mole, abortion, uterine fibrosis, abnormal saccarometabolism, abnormal lipidmetabolism or oxytocin.

XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 172; DB 20; Length 31,
Best Local Similarity 100.0%; Pred. No. 3.9e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRANOHSMERITPDPINPAWYAGRGRIPVGRF 31
Db 1 strabghsmeirtpdpinpaawgrrgripvrf 31

RESULT 3
W87613

ID W87613 standard; Peptide; 31 AA.
XX
AC
XX
DT 29-MAR-1999 (first entry)

DE Bovine 19P2 ligand.
XX
KW 19P2 ligand; G Protein coupled receptor; Pituitary; prolactin releasing peptide; cattle; dementia; breast cancer; KW therapy.

OS Bos taurus.

PN EP887117-A2.
XX
PD 30-DEC-1998.

PP 25-JUN-1998; 98EP-0111725.

XX
PR 27-JUN-1997; 97JP-017211B.

XX
PA (TAKE) TAKEDA CHEM IND LTD.

XX
PI Moriya T, Nishimura O, Suenaga M, Tanaka Y;

XX
DR WPI; 1999-047844/05.

DR WPI; 1999-105614/09.

XX
PT Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy

XX
PT Claim 3; Page 135; 241pp; English.

CC The present sequence represents a bovine pituitary-derived ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypoparathyroidism, gonocystic coagensis, menopausal syndrome, euthyroid or hypometabolism. They can be used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomata; brain tumour, emmenopathy, autoimmune disease, acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dysospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irrigation mole, abortion, uterine fibrosis, abnormal saccarometabolism, abnormal lipidmetabolism or oxytocin.

XX
SQ Sequence 31 AA;

XX
PT Producing a 19P2 pituitary G protein receptor ligand - by cleavage of a fusion protein useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease

XX
PT Claim 5; Page 34; 56pp; English.

XX
 CC This is the amino acid sequence of the bovine pituitary G
 CC protein-coupled receptor ligand 19P2L. A method suitable for
 CC commercial high-level production of 19P2L comprises expressing
 CC the ligand in host cells as a recombinant fusion protein e.g. with
 CC human basic fibroblast growth factor (see V83792-93) that has
 CC been modified to include an N-terminal cysteine residue. The
 CC ligand is released from the fusion by cyanulation followed by
 CC ammonolysis. 19P2L has prolactin secretion-inhibiting properties.
 CC It can be used in the treatment and prevention of various diseases including:
 CC senile dementia, cerebrovascular dementia, and dementia associated
 CC with: neurological disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease, Pick's disease, Huntington's disease), infectious diseases
 CC (e.g. Creutzfeld-Jakob's), endocrine or metabolic disease or
 CC toxicosis (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism,
 CC intoxication by drugs, metal and organic compounds), tumourigenic
 CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
 CC subarachnoidal haemorrhage, and other types of dementia, depression,
 CC hyperactive child syndrome (microencephalopathy) and disturbance of
 CC consciousness. It is also useful for prevention and treatment of
 CC diseases associated with prolactin hypo and hypersecretion
 CC respectively, including: hyperprolactinaemia, pituitary adenoma,
 CC breast cancer, infertility, impotence and autoimmune disease
 CC (hypopituitarism, osteoporosis, menopausal syndrome and renal failure (hyposecretion
 CC disorders). The 19P2 polypeptide/amide is also useful as a test
 CC reagent for study of the prolectin secretory function or as a
 CC lactogogue in mammalian farm animals.

XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 172; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3. 9e-19; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 0; ID 0; Gaps 0;
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 Db 1 srahqhsmeirtpdinpawwagrgripvgf 31

RESULT 4
 W95188

ID W95188 standard; peptide; 31 AA.
 AC W95188;
 XX DT 10-MAR-1999 (first entry)

DE Bovine pituitary-derived ligand polypeptide fragment.

XX Pituitary-derived ligand polypeptide; G protein coupled orphan receptor;
 KW GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
 KW tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
 KW Alzheimer's disease; Parkinson's disease; drug;
 KW Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
 KW secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
 KW gene therapy; transgenic animal; bovine.

OS Bos sp.

XX W09849295-A1.

XX 05-NOV-1998.

XX 27-APR-1998; 98WO-JP01923.

XX 28-APR-1997; 97JP-0109974.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Fukusumi S, Hinuma S;

XX DR WPI; 1999-009423/01.

XX PR New polypeptide ligand for orphan G protein coupled receptors - used
 PR for treating disorders of central nervous system, pituitary and
 PR pancreas, and for drug screening.

XX PS Example 19: Page 150; 206pp; English.

XX
 CC The invention relates to a murine pituitary-derived ligand polypeptide
 CC which is a ligand for the G-protein coupled orphan receptor designated
 CC SP10 (human) or UHR-1 (rat). Cells transformed with a vector containing
 CC the ligand polypeptide encoding DNA are used to produce a recombinant
 CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate
 CC function of the pituitary, central nervous system, pancreas and other
 CC tissues and can be used to screen for agents that modulate binding of the
 CC polypeptide to the receptor; to quantify the amount of receptor in a
 CC sample and to raise antibodies. They may also be used therapeutically,
 CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's
 CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
 CC diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
 CC rheumatoid arthritis; epilepsy and many others; also to improve post-
 CC operative nutritional status and as vasopenics. Transgenic animals
 CC carrying the ligand polypeptide encoding DNA or its mutant are used to
 CC study the function of the polypeptide-expressing genes, as models of
 CC disease, for drug screening and as source of cell lines. The ligand
 CC polypeptide DNA is used as a source of probes and primers; to identify
 CC related sequences; in receptor-binding assays; for production of Ab and
 CC antisera; in drug development; for gene therapy and to develop transgenic
 CC animals. The present sequence represents a bovine genome-derived ligand
 XX polypeptide fragment which is similar to the murine ligand-polypeptide.

XX SQ Sequence 31 AA;

Query Match 100.0%; Score 172; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3. 9e-19; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 0; ID 0; Gaps 0;
 QY 1 SRAHQHSMETRPPDINPAWWAGRGRIPVGRF 31
 Db 1 srahqhsmeirtpdinpawwagrgripvgf 31

RESULT 5
 B10347

ID B10347 standard; peptide; 31 AA.
 AC B10347;
 XX DT 24-NOV-2000 (first entry)

DE Bovine oxytocin secretion promoting peptide SEQ ID NO: 3.

XX Bovine; oxytocin secretion promoter; G protein-coupled receptor protein;
 KW Bovine; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
 KW caesarean section; artificial fertilization; galactostasis; goat; pig;
 KW veterinary medicine; milk production.

XX OS Bos taurus.

XX WO200038704-A1.

XX 06-JUL-2000.

XX 22-DEC-1999; 99WO-JP07199.

XX 25-DEC-1998; 98JP-0369585.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Matsumoto H, Kitada C, Hinuma S;

DR WPI; 2000-452298/39.

XX
 CC Physiologically-active polypeptide recognized as ligand by G protein coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.

XX
 PS Claim 3; Page 50; 72pp; Japanese.

CC This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g., weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion promoter.

XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 172; DB 21; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3. 9e-19;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SRAHQHSMETRPINPANWAGRGRPVGRF 31.
 ||||| ||||| ||||| ||||| |||||
 Db 1 srahqhsmetrpindpawgagrirgvgrf 31.

RESULT 6
 Y49290 ID Y49290 standard; peptide; 31 AA.
 XX AC Y49290;
 XX DT 22-FEB-2000 (first entry)
 XX DE 19P2 ligand peptide fragment.

XX KW Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.
 XX OS Homo sapiens.
 XX FH Key
 FT Modified-site Location/Qualifiers
 /note= "C-terminal amide"
 XX PN WO9960112-A1.
 XX PD 25-NOV-1999.
 XX PP 20-MAY-1999; 99WO-JP02650.
 XX PR 21-MAY-1998; 98JP-0140293.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Matsumoto H, Kitada C, Hinuma S;
 XX DR WPI; 2000-039381/03.
 XX PS New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality

XX Disclosure; Page 27; 73pp; Japanese.
 XX The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences Y49290-302 represent peptide fragments of the 19P2 ligand.

XX SQ Sequence 31 AA;

CC prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences Y49290-302 represent peptide fragments of the 19P2 ligand.

Query Match 100.0%; Score 172; DB 21; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3. 9e-19;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SRAHQHSMETRPINPANWAGRGRPVGRF 31.
 ||||| ||||| ||||| |||||
 Db 1 srahqhsmetrpindpawgagrirgvgrf 31.

SQ Sequence 31 AA;

XX
 CC The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or its

Query Match Score 172; DB 18; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.1e-19;
 Matches 31; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Query Match Score 172; DB 20; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.1e-19;

RESULT 8
 W31372 standard; peptide; 32 AA.
 W31372;
 XX
 DT 06-APR-1998 (first entry)
 XX
 DE Bovine G protein-coupled receptor ligand peptide fragment 2.
 XX
 KW G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.
 XX
 OS Bos taurus.
 XX
 PN W09724436-A2.
 XX
 PD 10-JUL-1997.
 XX
 PF 96WO-JP03821.
 XX
 PR 18-SEP-1996; 96JP-0246573.
 PR 28-DEC-1995; 95JP-0343271.
 PR 15-MAR-1996; 96JP-0059119.
 PR 12-AUG-1996; 96JP-0211805.
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
 PI Kawamata Y, Kitada C;
 XX
 DR WPI, 1997-363672/33.
 XX
 DR N-PSDB; V02395.
 PT Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
 PT XX
 PS Claim 2; Page 160-161; 258pp; English.
 CC This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 23 to 54 of the sequence in W31368 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and hypophagia, hypercholesterolaemia, hyperglycaemia, hyperlipidaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, rheumatoid arthritis, spinal injury, transient brain ischaemia, amyotrophic lateral sclerosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility and/or oligoagalmia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
 CC Sequence 32 AA;
 SQ XX

Query Match Score 172; DB 18; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.1e-19;
 Matches 31; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Query Match Score 172; DB 20; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.1e-19;

RESULT 9
 W095189 standard; peptide; 32 AA.
 W095189;
 XX
 AC W095189,
 DT 10-MAR-1999 (first entry)
 XX
 DE Bovine pituitary-derived ligand polypeptide fragment.
 XX
 KW Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.
 XX
 OS Bos sp.
 XX
 PN W09849295-A1.
 XX
 PD 05-NOV-1998.
 XX
 PR 27-APR-1998; 98WO-JP01923.
 XX
 PR 28-APR-1997; 97JP-0109974.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukusumi S, Hinuma S;
 XX
 DR WPI; 1999-009423/01.
 XX
 PR New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
 PT XX
 PS Example 19; Page 150; 205pp; English.
 CC The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis; epilepsy and many others, also to improve post-operative nutritional status and as vasoconstrictor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences, in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide.
 CC Sequence 32 AA;

DT 10-MAR-1999 (first entry)
 XX
 DE Bovine pituitary-derived ligand polypeptide fragment.
 XX
 KW Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
 KW GPR10; UHR11; modulator; pituitary; central nervous system; pancreas;
 KW tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
 KW Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
 KW gene therapy; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
 KW transgenic animal; bovine.
 XX
 OS Bos sp.
 XX
 PN WO9849295-A1.
 XX
 DD 05-NOV-1998.
 XX
 PF 27-APR-1998; 98WO-JP01923.
 XX
 PR 28-APR-1997; 97JP-0109974.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukumumi S, Hinuma S;
 XX
 DR WPI; 1999-009423/01.
 XX
 PT New polypeptide ligand for orphan G protein coupled receptors - used
 PT for treating disorders of central nervous system, pituitary and
 PT pancreas, and for drug screening
 XX
 Example 19; Page 150; 206pp; English.
 PS
 XX
 CC The invention relates to a murine pituitary-derived ligand polypeptide,
 CC which is a ligand for the G-protein coupled orphan receptor designated
 CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
 CC the ligand polypeptide encoding DNA are used to produce a recombinant
 CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate
 CC function of the pituitary, central nervous system, pancreas and other
 CC tissues and can be used to screen for agents that modulate binding of the
 CC polypeptide to the receptor; to quantify the amount of receptor in a
 sample and to raise antibodies. They may also be used therapeutically,
 e.g. to treat senile dementia, Alzheimer's, Parkinson's or Huntington's
 diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
 CC diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
 CC rheumatoid arthritis; epilepsy; and many others, also to improve post-
 CC operative nutritional status and as vasoconstrictor. Transgenic animals
 CC carrying the ligand polypeptide encoding DNA or its mutein are used to
 study the function of the polypeptide-expressing genes, as models of
 CC disease, for drug screening and as source of cell lines. The ligand
 CC polypeptide DNA is used as a source of probes and primers; to identify
 CC related sequences; in receptor-binding assays; for production of Ab and
 CC antisera; in drug development; for gene therapy and to develop transgenic
 CC animals. The present sequence represents a bovine genome-derived ligand
 CC polypeptide fragment which is similar to the murine ligand-polypeptide.
 XX
 Sequence 33 AA;

RESULT 14
 Y49297
 ID Y49297 standard; peptide; 33 AA.
 XX
 AC B10349;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Bovine oxytocin secretion promoting peptide SEQ ID NO: 5.
 XX
 Bovine oxytocin secretion promoter; G protein-coupled receptor protein;
 KW treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
 KW cesarean section; artificial fertilization; galactostasis; goat; pig;
 KW veterinary medicine; milk production.
 XX
 OS Bos taurus.
 XX
 PN WO200038704-A1.
 XX
 PD 06-JUL-2000.
 XX
 PF 22-DEC-1999; 99WO-JP07199.
 XX
 PR 25-DEC-1998; 98JP-0369585.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Matsumoto H, Kitada C, Hinuma S;
 XX
 DR WPI; 2000-452298/39.
 XX
 PT Physiologically-active polypeptide recognized as ligand by G
 PT protein-coupled receptor protein, for promoting secretion of oxytocin,
 PT as drugs for diseases relating to oxytocin secretion and in veterinary
 PT medicine -
 XX
 PS Disclosure; Page 51; 72pp; Japanese.

XX
 CC This invention describes a novel oxytocin secretion-regulating agent
 CC which contains a ligand peptide or its salt for the G protein-coupled
 receptor protein. It is useful in the form of drugs for ameliorating,
 CC preventing and treating diseases relating to oxytocin secretion e.g.,
 CC weak pains and atonic bleeding, before and after expulsion of placenta,
 CC uterine recovery failure, caesarean section, stoppage of artificial
 CC fertilization or galactostasis and is also applicable in veterinary
 CC medicine for promoting milk production in cow, goat and pig. This
 CC sequence represents a bovine peptide which acts as an oxytocin secretion
 CC promoter.
 XX
 SQ Sequence 33 AA;

Query Match 100.0%; Score 172; DB 20; Length 33;
 Best Local Similarity 100.0%; Pred No. 4.2e-19; Indels 0; Gaps 0;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHQHSMETRDPDINPAWYAGRCIRPVGRF 31
 DB 1 srahqhsmeirtpdinpawayagr9irpvgrf 31

RESULT 14
 Y49297
 ID Y49297 standard; peptide; 33 AA.
 XX
 AC Y49297;
 XX
 DT 22-FEB-2000 (first entry)
 XX
 DE 19P2 ligand peptide fragment.
 XX
 KW Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
 KW pituitary; regulatory mechanism; central nervous system; pancreatic.
 XX
 OS Bos sp.
 XX
 PN WO960112-A1.

RESULT 13
 B10349 standard; peptide; 33 AA.
 ID B10349
 XX

XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-JP02650.
PR XX
21-MAY-1998; 98JP-0140233.
PA XX
(TAKE) TAKEDA CHEM IND LTD.
XX
PT Matsumoto H, Kitada C, Hinuma S;
XX
WPI; 2000-039381/03.

New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality disclosure; Page 27; 73pp; Japanese.

The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19p2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences Y49290-302 represent peptide fragments of the 19p2 ligand.

SQ Sequence 33 AA;

Query Match 100.0%; Score 172; DB 21; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.2e-19; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRRAHQHSMEIRTPDINPAWVAGRGIRPVGRF 31
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 srahqhsmeirtpdinpawvagrgirgvgrf 31

XX
Sequence 98 AA;

Query Match 100.0%; Score 172; DB 18; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-18; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRRAHQHSMEIRTPDINPAWVAGRGIRPVGRF 31
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 srahqhsmeirtpdinpawvagrgirgvgrf 53

Search completed: April 17, 2001, 15:38:41
Job time: 348 sec

RESULT 15
W31382 ID W31382 standard; Protein: 98 AA.
AC XX
M31382;
CC XX
DT 06-APR-1998 (first entry)
XX
DE Bovine genome derived G protein-coupled receptor ligand.
XX
KW G protein coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.
XX
OS Bos taurus.
XX
PN WO9724436-A2.
PD 10-JUL-1997.
XX
PF 26-DEC-1996; 96WO-JP02821.
XX
PR 18-SEP-1996; 96JP-0246573.
PR 28-DEC-1995; 95JP-0343371.
PR 15-MAR-1996; 96JP-0053419.
PR 12-AUG-1996; 96JP-0211805.
PA XX
(TAKE) TAKEDA CHEM IND LTD.
XX
FUji R, Fukumi S, Habata Y, Hinuma S, Hosoya M;
PI Kawama Y, Kitada C;
XX
WPI; 1597-36367/33.

Query Match 31.7%; Score 34.5; DB 2; Length 503;
 Best Local Similarity 36.7%; Pred. No. 3; 5;
 Matches 11; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

1 SRAHQHSMERITPDINPAWYAGRGIRGVGR 30
 | : | : | : | : | : | : | : | : | : | : | : | : | : |
 435 SSSASHSVELDITQAR-EWFMDRDVPEGO 463

Alternate names: hypothetical protein YOR253W - yeast (*Saccharomyces cerevisiae*)
 Species: *Saccharomyces cerevisiae*
 Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Nov-1999
 Accession: S67150
 Genetics: MPR5:YOR253W
 Gene: MPR5:YOR253W
 Map position: 15R

Reference number: S67143
 Accession: S67150
 Molecule type: DNA
 Residues: 1-176 <XRD>
 Cross-references: EMBL:Z75161; NID:91420572; PID:e252411; PID:91420573; GSPDB:GN00015;
 Experimental source: strain S288C
 Jauniaux, J.C.; Poirey, R.
 Submitted to the Protein Sequence Database, July 1996

Query Match 31.1%; Score 53.5; DB 2; Length 175;
 Best Local Similarity 31.2%; Pred. No. 1.6; 5;
 Matches 10; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

1 SRAHQHSMERITPDINPAWYAGRGIRGV 29
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 120 SECHQHNWVFLPAPVDDLTQWFLHGFPGV 151

SULT 4
 5580
 enine deaminase-related protein - *Deinococcus radiodurans* (strain R1)
 Species: *Deinococcus radiodurans*
 Accession: C75580
 Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vaithyanathan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 ; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 ience 286, 1571-1577, 1999
 Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 Reference number: A72250; MUID:20036896
 Accession: C75580
 Status: preliminary
 Molecule type: DNA
 Residues: 1-376 <XRD>
 Cross-references: GB:AE001863; GB:AE001825; NID:96460670; PIDN:AAF12376.1; PID:9646067
 Experimental source: strain R1
 Genetics: MPR5:YOR253W
 Gene: DRA026B
 Map position: 2

RESULT 5
 F83376
 conserved hypothetical protein PA2151 [Imported] - *Pseudomonas aeruginosa* (strain PAO
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 R;Accession: F83376
 Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pa
 A;Reference number: AB2950; MUID:2043737
 A;Accession: F83376
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-664 <STO>
 A;Cross-references: GB:AE004642; GB:AE004091; NID:99948163; PIDN:AAG05539.1; GSPDB:GN
 C;Experimental source: strain PAO1
 C;Genetics:
 A;Gene: PA2151

RESULT 6
 F83376
 conserved hypothetical protein PA2151 [Imported] - *Pseudomonas aeruginosa* (strain PAO
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 R;Accession: F83376
 Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pa
 A;Reference number: AB2950; MUID:2043737
 A;Accession: F83376
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-664 <STO>
 A;Cross-references: GB:AE004642; GB:AE004091; NID:99948163; PIDN:AAG05539.1; GSPDB:GN
 C;Experimental source: strain PAO1
 C;Genetics:
 A;Gene: PA2151

RESULT 7
 T21075
 hypothetical protein F19H6.1 - *caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
 C;Accession: T21075; T21124
 Murray, A.; McMurtry, A.
 Submitted to the EMBL Data Library, August 1995
 A;Reference number: Z19368
 A;Accession: T21075
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-294 <WIL>
 A;Cross-references: EMBL:Z50873; PIDN:CAA90762.1; GSPDB:GN00028; CESP:F19H6.1

RESULT 12

Qy 4 RQHSMETRTPDINPAWAGRGRGIRPVGF 31
 C;Species: *Caenorhabditis elegans*
 C;Accession: T33175
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 R;Greco, T.; Bradshaw, H.; Kepler, D.
 Submitted to the EMBL Data Library, May 1998
 A;Description: The sequence of *C. elegans* cosmid C24G6.
 A;Reference number: 221298
 A;Accession: T33175
 A;Status: preliminary; translated from GB/EMBL/DBAJ
 A;Molecule type: DNA
 A;Residues: 1-527 <GRE>
 A;Cross-references: EMBL:AF067936; PIDN: AAC19213_1; GSPDB:GN00023; CESP:C24G6_6
 A;Experimental source: strain Bristol N2; clone C24G6
 C;Genetics:
 A;Gene: CESP:C24G6_6
 A;Map position: 5
 A;Introns: 20/3; 77/1; 129/2; 208/3; 470/2

Query Match 29.1%; Score 50; DB 2; Length 527;
Best Local Similarity 66.7%; Pred. No. 17; Mismatches 8; Conservative 2; Indels 0; Gaps 0;

Qy 13 PDINPAWAGR 24
 I:: |||||
 Db 370 PNVLSAWAGKG 381

RESULT 13

S76955 hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
 C;Species: *Synechocystis* sp.
 A;Variety: PCC 6803
 C;Accession: 22-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C;Accession: S76955
 C;Accession: 22-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 R;Kanako, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3: 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
 A;Reference number: S74322; MUID:97061201
 A;Accession: S76955
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-128 <GRE>
 A;Cross-references: EMBL:D90917; GB:AB001339; NID:gi:1653836; PIDN:BAAL18867_1; PID:di101960
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 28.5%; Score 49; DB 2; Length 128;
Best Local Similarity 33.3%; Pred. No. 5.2; Mismatches 11; Conservative 5; Indels 13; Gaps 4; Gaps 1;

Qy 1 SRQHSMETRTPDINPAWAGR--GIRPVGF 29
 I:: || : || | : || | : || |
 Db 11 SPENNQSLDCSSPRSPRSKQARFSEGTTPTG 43

RESULT 14

S76814 hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
 C;Species: *Synechocystis* sp.
 A;Variety: PCC 6803

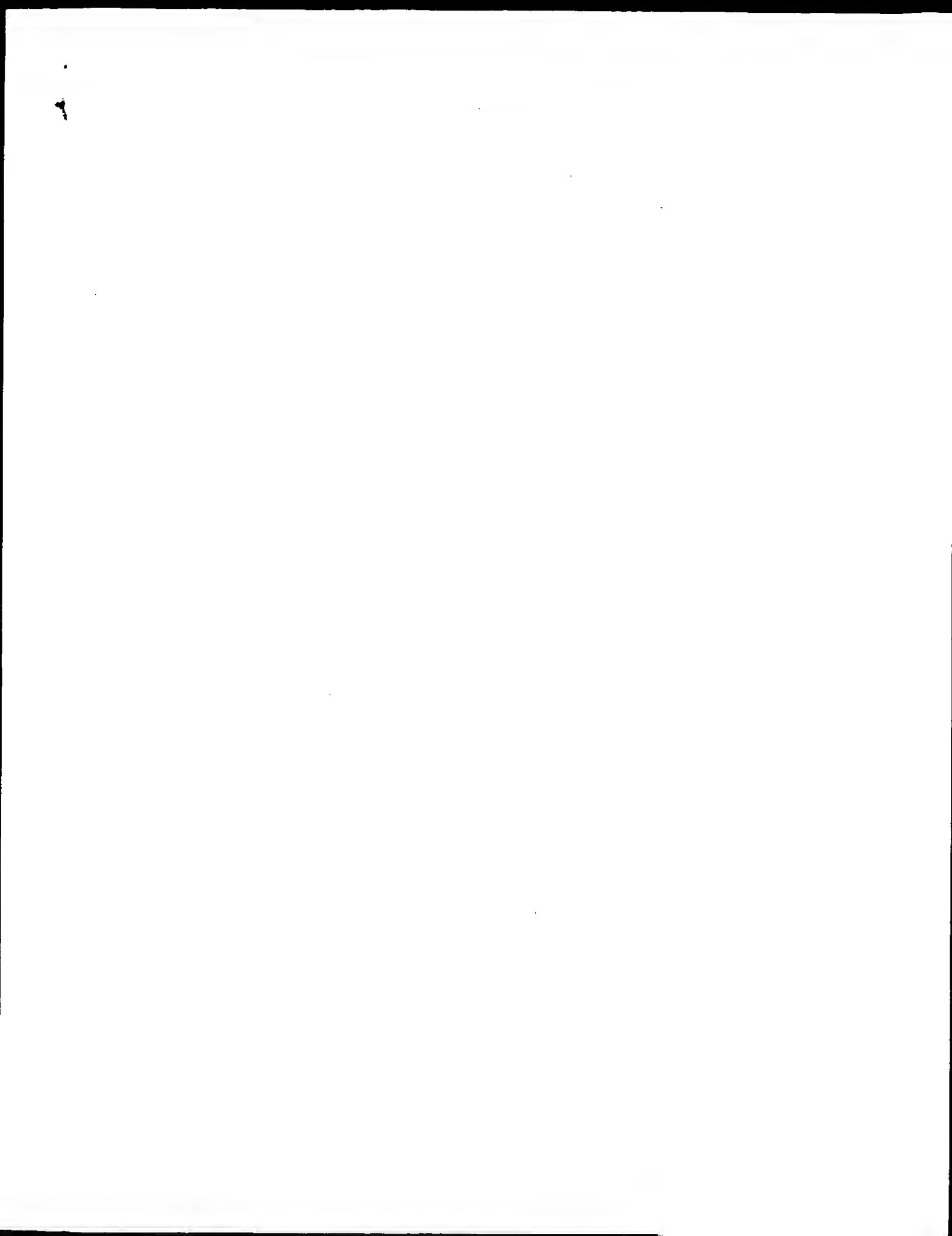
Query Match 28.2%; Score 48.5; DB 2; Length 548;
Best Local Similarity 35.5%; Pred. No. 30; Mismatches 11; Conservative 3; Indels 10; Gaps 7; Gaps 1;

Qy 1 SRHQ-----HSMEIRTPDINPAWAGR 24
 I : || | : || | : || | : || |
 Db 118 SLIDHSPMHFLHLPLQHSPFHOPSHWGRG 148

Search completed: April 17, 2001, 15:45:51
 Job time: 599 sec

Tue Apr 17 15:46:14 2001

us-09-446-543a-5.rpr



GenCore version 4.5
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OM protein - protein search, using sw model

Run on : April 17, 2001, 15:38:41 ; Search time 116.94 Seconds

(without alignments)

9.777 Million cell updates/sec

Title: US-09-446-543A-8
Perfect score: 115
Sequence: TPDINPAWYAGRGRGIRPNVGRP 20

Scoring table: BLOSUM62

Gpop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters:

390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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16: /SIDS1/gcdata/geneseq/geneseq/AA1995.DAT:*

17: /SIDS1/gcdata/geneseq/geneseq/AA1996.DAT:*

18: /SIDS1/gcdata/geneseq/geneseq/AA1997.DAT:*

19: /SIDS1/gcdata/geneseq/geneseq/AA1998.DAT:*

20: /SIDS1/gcdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDS1/gcdata/geneseq/geneseq/AA2000.DAT:*

22: /SIDS1/gcdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	115	100.0	20	W31374
2	115	100.0	20	W97232
3	115	100.0	20	W55191
4	115	100.0	20	B0350
5	115	100.0	20	Y9301
6	115	100.0	21	W01375
7	115	100.0	21	W55192
8	115	100.0	21	B0351
9	115	100.0	22	W31376
10	115	100.0	22	W55193
11	115	100.0	22	B10352

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT	1	
W31374		
ID	W31374	standard; Peptide; 20 AA.
XX		
AC	W31374;	
XX		
DT	06-APR-1998	(first entry)
XX		
DE	Bovine G protein-coupled receptor ligand peptide fragment 4.	
XX		
KW	G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.	
KW		
OS	Bos taurus.	
XX		
PN	WO9724436-A2.	
XX		
PD	10-JUL-1997.	
XX		
PF	26-DEC-1996; 96WO-JP03821.	
XX		
PR	18-SEP-1996; 96JP-0245573.	
PR	28-DEC-1995; 95JP-043371.	
PR	15-MAR-1996; 96JP-005419.	
PR	12-APR-1996; 96JP-0211805.	
XX		
PA	(TAKE) TAKEDA CHEM IND LTD.	
XX		
PI	Fuji R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;	
PI	Kawamura Y, Kitada C;	
XX		
DR	wpi: 1997-363672/33.	
NPDB; V02397.		

XX
 PT Ligand peptide for G protein-coupled receptor - acts by modulating
 function in the central nervous system, pancreas and pituitary gland
 XX
 PS claim 2; Page 161; 258pp; English.
 XX
 CC This sequence represents a peptide fragment of a novel bovine pituitary
 derived ligand corresponding to amino acid residues 34 to 53 of the
 sequence in WO1368 and is used in an assay to monitor ligand binding to
 the G protein-coupled receptor protein. Pharmaceutical compositions
 containing this ligand may be used as a pituitary function modulator, a
 central nervous system modulator or a pancreatic function modulator. This
 ligand could have specific applications as a prophylactic or therapeutic
 agent for dementia, depression, hypokinetic syndrome, disturbance of
 consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone
 secretory disease, hyper- and polyphagia, hypercholesterolaemia,
 hyperglycideraemia, hyperlipidaemia, hyperprolactinaemia, diabetes,
 cancer, pancreatitis, renal disease, Turner's syndrome, neurosis,
 rheumatoid arthritis, spinal injury, transient brain ischaemia,
 amyotrophic lateral sclerosis, acute myocardial infarction,
 spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
 osteoporosis, asthma, epilepsy, infertility and/or oligogalactia. Assays
 can also be developed to screen compounds which are capable of altering
 the binding activity of the ligand thus affecting activation of the G
 protein-coupled receptor protein.
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 115; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.7e-12; Mismatches 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;
 Oy 1 TPDINPAWAGRGTRPWF 20
 Db 1 tpdinpawagrgtrpwf 20

DR WPI; 1999-105614/09.
 XX Use of G protein-coupled receptor ligands - for modulating prolactin
 secretion or placental function, e.g. for treating menopausal
 syndrome, tumours, autoimmune disease or abnormal pregnancy
 XX
 PS claim 3; Page 136; 241pp; English.
 XX
 CC The present sequence represents a bovine pituitary-derived ligand
 fragment. It is used in the course of the invention. The specification
 describes an agent for modulating prolactin secretion which comprises a
 ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
 protein. The agents for promoting prolactin secretion can be used for
 treating or preventing hypoprolactinism, gynaecological, menopausal
 lactation in a domestic mammal and as an aphrodisiac. The agents for
 inhibiting prolactin secretion can be used for treating or preventing
 pituitary adenomatosis, brain tumour, emmenoptysis, autoimmune disease,
 prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
 acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome,
 Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dysospermia.
 CC The inhibitory agents can also be used as contraceptives. The agents for
 modulating placental function can be used for treating or preventing
 choriocarcinoma, hydatid mole, eruptive mole, abortion, uterine fibroid fetus,
 CC abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 115; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.7e-12; Mismatches 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;
 Oy 1 TPDINPAWAGRGTRPWF 20
 Db 1 tpdinpawagrgtrpwf 20

RESULT 2
 W9732
 ID W9732 standard; peptide; 20 AA.
 XX
 AC W9732;
 DT 06-MAY-1999 (first entry)

DE Bovine pituitary-derived ligand polypeptide fragment.
 XX
 KW Bovine pituitary-derived ligand; modulation; prolactin secretion;
 KW G protein-coupled receptor; GPCR; hypoovarianism; gonocystic carcinogenesis;
 KW menoapausal syndrome; euthyroid; hypometabolism; lactation;
 KW pituitary adenomas; brain tumour; emmenoptysis; autoimmune disease;
 KW prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
 KW acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome;
 KW Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dysospermia;
 KW contraceptive; placental function; choriocarcinoma; hydatid mole;
 KW irrigation mole; abortion; untrophic fetus; abnormal saccharometabolism;
 KW abnormal lipiddemabolism; oxytocia.
 XX
 OS Bos sp.
 XX
 PN W09858962-A1.

XX
 PD 30-DEC-1998.
 XX
 PF 22-JUN-1998; 98WO-JP02765.

PR 23-JUN-1997; 97JP-0165437.
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fujii R., Hinuma S., Kawamata Y., Matsumoto H;
 XX

DR WPI; 1999-105614/09.
 XX Use of G protein-coupled receptor ligands - for modulating prolactin
 secretion or placental function, e.g. for treating menopausal
 syndrome, tumours, autoimmune disease or abnormal pregnancy
 XX
 PS claim 3; Page 136; 241pp; English.
 XX
 CC The present sequence represents a bovine pituitary-derived ligand
 fragment. It is used in the course of the invention. The specification
 describes an agent for modulating prolactin secretion which comprises a
 ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
 protein. The agents for promoting prolactin secretion can be used for
 treating or preventing hypoprolactinism, gynaecological, menopausal
 lactation in a domestic mammal and as an aphrodisiac. The agents for
 inhibiting prolactin secretion can be used for treating or preventing
 pituitary adenomatosis, brain tumour, emmenoptysis, autoimmune disease,
 prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
 acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome,
 Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dysospermia.
 CC The inhibitory agents can also be used as contraceptives. The agents for
 modulating placental function can be used for treating or preventing
 choriocarcinoma, hydatid mole, eruptive mole, abortion, uterine fibroid fetus,
 CC abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 115; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.7e-12; Mismatches 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;
 Oy 1 TPDINPAWAGRGTRPWF 20
 Db 1 tpdinpawagrgtrpwf 20

RESULT 3
 W95191
 ID W95191 standard; peptide; 20 AA.
 XX
 AC W95191;
 DT 10-MAR-1999 (first entry)

DE Bovine pituitary-derived ligand polypeptide fragment.
 XX
 KW pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
 KW GPR10; USH-1; modulator; pituitary; central nervous system; pancreas;
 KW tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
 KW Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
 KW secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasoconstrictor;
 KW gene therapy; transgenic animal; bovine.
 XX
 OS Bos sp.
 XX
 PN W09849295-A1.

XX
 PD 05-NOV-1998.
 XX
 PF 27-APR-1998; 98WO-JP01923.

XX
 PR 28-APR-1997; 97JP-0169974.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukumui S., Hinuma S.;
 XX
 DR 1998-009423/01.

DR New polypeptide ligand for orphan G protein coupled receptors - used

PT for treating disorders of central nervous system; pituitary and
 PT pancreas, and for drug screening
 XX
 PS Example 19; Page 151; 206pp; English.

XX The invention relates to a murine pituitary-derived ligand polypeptide
 CC which is a ligand for the G-protein coupled orphan receptor designated
 GPR10 (human) or UMR-1 (rat). Cells transformed with a vector containing
 the ligand polypeptide encoding DNA are used to produce a recombinant
 ligand polypeptide. The ligand polypeptide, and its fragments, modulate
 function of the pituitary, central nervous system, pancreas and other
 tissues and can be used to screen for agents that modulate binding of the
 polypeptide to the receptor; to quantify the amount of receptor in a
 sample and to raise antibodies. They may also be used therapeutically,
 e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's
 diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
 diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
 rheumatic arthritis; epilepsy and many others, also to improve post-
 operative nutritional status and as vasoconstrictor. Transgenic animals
 carrying the ligand polypeptide encoding DNA or its mutant are used to
 study the function of the polypeptide-expressing genes, as models of
 disease, for drug screening and as source of cell lines. The ligand
 polypeptide DNA is used as a source of probes and primers; to identify
 related sequences, in receptor-binding assays, for production of Ab and
 antisera; in drug development; for gene therapy and to develop transgenic
 animals. The present sequence represents a bovine genome-derived ligand
 polypeptide fragment which is similar to the murine ligand-polypeptide.
 XX

SEQ Sequence 20 AA:

Query Match 100%; Score 115; DB 20; Length 20;
 Best Local Similarity 100%; Pred. No. 7; 7e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPDINPAPWAGRGIRGVGRF 20
 Db 1 tpdinpawgagrgrlrvgrf 20

RESULT 4

ID B10350 standard; peptide; 20 AA.

AC B10350;

XX DT 24-NOV-2000 (first entry)

XX DE Bovine oxytocin secretion promoting peptide SEQ ID NO: 6.

XX KW Bovine; oxytocin secretion promoter; G Protein-coupled receptor protein;
 treatment; disease; Pain; uterine recovery failure; cow;
 cesarean section; artificial fertilization; galactostasis;
 veterinary medicine; milk Production.

XX OS Bos taurus.

XX PN WO20038704-A1.

XX DD 06-JUL-2000.

XX PF 22-DEC-1999; 99WO-JP07199.

XX PR 25-DEC-1998; 98JP-0369585.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Matsumoto H, Kitada C, Hinuma S;

XX DR WPI; 2000-039381/03.

XX PT New monoclonal antibodies, useful in diagnosis, as drugs and in
 PT studying diseases related to ligand abnormality
 XX Disclosure; Page 27; 73pp; Japanese.

XX The invention provides a monoclonal antibody which has a specific
 CC reaction with the part peptide of the C-terminal of 19p2 ligand or its
 CC derivative. The antibodies can be used in diagnosis or to treat or
 prevent diseases associated with abnormality in the Pituitary function
 CC regulatory mechanism (e.g. promotion of prolactin secretion), central
 CC nervous regulatory mechanism, and pancreatic function regulatory
 mechanism. The antibody-based immunoassay can also be applied in

CC

PR as drugs for diseases relating to oxytocin secretion and in veterinary
 PT medicine

XX Claim 5; Page 51; 72pp; Japanese.

XX This invention describes a novel oxytocin secretion-regulating agent
 CC which contains a ligand peptide or its salt for the G protein-coupled
 receptor protein. It is useful in the form of drugs for ameliorating,
 CC preventing and treating diseases relating to oxytocin secretion e.g.,
 weak pains and atonic bleeding, before and after expulsion of placenta,
 CC uterine recovery failure, caesarean section, stoppage of artificial
 CC fertilization or galactorrhea and is also applicable in veterinary
 CC medicine for promoting milk production in cow, goat and pig. This
 CC sequence represents a bovine peptide which acts as an oxytocin secretion
 CC promotor.

SEQ Sequence 20 AA:

Query Match 100.0%; Score 115; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7; 7e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPDINPAPWAGRGIRGVGRF 20
 Db 1 tpdinpawgagrgrlrvgrf 20

RESULT 5

ID Y49301
 AC Y49301;

XX DT 22-FEB-2000 (first entry)

XX DE 19p2 ligand peptide fragment.

XX KW Monoclonal antibody; 19p2 ligand; diagnosis; prolactin secretion;
 KW pituitary; regulatory mechanism; central nervous system; pancreatic.
 XX OS Bos sp.

XX FH Key Location/Qualifiers

FT Modified-site 20
 FT /note= "C-terminal amide"

XX FN WO9960112-A1.

XX PD 25-NOV-1999.

XX PF 20-MAY-1999; 99WO-JP02650.

XX PR 21-MAY-1998; 98JP-0140293.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Matsumoto H, Kitada C, Hinuma S;

XX DR WPI; 2000-039381/03.

XX PT New monoclonal antibodies, useful in diagnosis, as drugs and in
 PT studying diseases related to ligand abnormality
 XX Disclosure; Page 27; 73pp; Japanese.

XX The invention provides a monoclonal antibody which has a specific
 CC reaction with the part peptide of the C-terminal of 19p2 ligand or its
 CC derivative. The antibodies can be used in diagnosis or to treat or
 prevent diseases associated with abnormality in the Pituitary function
 CC regulatory mechanism (e.g. promotion of prolactin secretion), central
 CC nervous regulatory mechanism, and pancreatic function regulatory
 mechanism. The antibody-based immunoassay can also be applied in

CC

clarifying the physiological functions of the ligand and its derivative. Sequences Y49290-302 represent peptide fragments of the 19p2 ligand.

CC clarifying the physiological functions of the ligand and its derivative
CC Sequences Y492G-302 represent peptide fragments of the 19p2 ligand.
XX

CC protein-coupled receptor protein.
XX
SO Sequence 21 AA:

Query Match 100.0%; Score 115; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.7e-12;
 Matches 20; Conservative 0; Mismatches 0;
 Qy 1 TPDINPAWYAGRGIRPYGRF 20
 Db 1 TPDINPAWYAGRGIRPYGRF 20

```

Query Match          100.0%;  Score 115;  DB 18;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 8 1e-12;
Matches 20;  Conservative 0;  Mismatches 0;  Indexes 0;
OY      1 TPDIINPAWKAGGRGPWGRF 20
||||||| ||||||| ||||| |
Db      1 tpdinpawyaggrgpwgrf 20

```

XX DE
 KW Bovine G protein-coupled receptor ligand peptide fragment 5.
 KW G protein-coupled receptor; ligand binding; pharmaceutical;
 KW modulator; pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.
 XX OS
 Bos taurus.
 XX PN WO9724436-A2.
 XX PPD
 10-JUL-1997.
 XX PE
 26-DEC-1996; 96W0-JP03821.
 XX PR 18-SEP-1996; 96JP-0246573.
 XX PR 28-DEC-1995; 95JP-0343371.
 XX PR 15-MAR-1996; 96JP-0059419.
 XX PR 12-AUG-1996; 96JP-0211805.
 XX DR PA (TAKE) TAKEDA CHEM IND LTD.
 XX PR Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
 XX PR Kawamata Y, Kitada C;
 XX WPI; 1997-36362/33.
 XX N-PSDB; V03398.
 XX PR Ligand peptide for G protein-coupled receptor - acts by modulating
 PR function in the central nervous system, pancreas and pituitary gland
 Claim 2; Page 162; 258pp; English.
 CC This sequence represents a peptide fragment of a novel bovine pituitary
 CC derived ligand corresponding to amino acid residues 34 to 54 of the
 CC sequence in W3368 and is used in an assay to monitor ligand binding to
 CC the G protein-coupled receptor protein. Pharmaceutical compositions
 CC containing this ligand may be used as a pituitary function modulator, a
 CC central nervous system modulator or a pancreatic function modulator. This
 CC ligand could have specific applications as a prophylactic or therapeutic
 CC agent for dementia, depression, hyperkinetic syndrome, disturbance of
 CC consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone
 CC secretory disease, hyper- and polyphagia, hypercholesterolaemia,
 CC hyperglycidaemia, hyperlipidaemia, hyperproctinaemia, diabetes,
 CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis,
 CC rheumatoid arthritis, spinal injury, transient brain ischaemia,
 CC amyotrophic lateral sclerosis, acute myocardial infarction,
 CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
 CC osteoporosis, asthma, epilepsy, impotency and/or oligogalactia. Assays
 CC can also be developed to screen compounds which are capable of altering
 CC the binding activity of the ligand thus affecting activation of the G

XX
 KW pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
 KW UHR-1; modulator; pituitary; central nervous system; pancreas;
 KW tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
 KW Cretzfelder-Jakob disease; poisoning; schizophrenia; growth hormone;
 KW secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasoressor;
 KW gene therapy; transgenic animal; bovine.
 XX
 OS Bos sp.
 XX PN WO9849295-A1.
 XX PD 05-NOV-1998.
 XX PF 27-APR-1998; 98WO-JP01923.
 XX PR 28-APR-1997; 97JP-0109974.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Fukusumi S, Hinuma S;
 XX DR WPI; 1999-009423/01.
 XX PT New polypeptide ligand for orphan G protein coupled receptors - used
 PT for treating disorders of central nervous system, pituitary and
 PT pancreas, and for drug screening
 XX PS Example 19: Page 151; 206pp; English.
 CC The invention relates to a murine pituitary-derived ligand polypeptide
 CC which is a ligand for the G-protein coupled orphan receptor designated
 CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
 CC the ligand polypeptide encoding DNA are used to produce a recombinant
 CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate
 CC function of the pituitary, central nervous system, pancreas and other
 CC tissues and can be used to screen for agents that modulate binding of the
 CC polypeptide to the receptor; to quantify the amount of receptor in a
 CC sample and to raise antibodies. They may also be used therapeutically,
 CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's
 CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
 CC diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
 CC rheumatoid arthritis; epilepsy and many others; also to improve post-
 CC operative nutritional status and as vasopressor. Transgenic animals
 CC carrying the ligand polypeptide encoding DNA or its mutant are used to
 CC study the function of the polypeptide-expressing genes, as models of
 CC disease, for drug screening and as source of cell lines. The ligand
 CC polypeptide DNA is used as a source of probes and primers; to identify
 CC related sequences; in receptor-binding assays; for production of Ab and

Page 5

CC antisera; in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide.

W31376 standard; Peptide: 22 AA.
ID: W31376

```

Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Queried sequence:      AC
Matched sequence:      M31376;
Matches 20;保守性 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPDINPAWVGRGIRGVGRF 20
||||||| ||||| ||||| ||||| |
Db 1 tpdlnpawvagrgrgvgrf 20

05-APR-1998 (first entry)
XX DT
XX DE Bovine G protein-coupled receptor ligand peptide fragment 6.
XX KW G protein-coupled receptor; ligand binding; pharmaceutical;
KW

```

RESULT **B**

mbourator, KW
therapeutic agent, KW
therapeutic

ID B10351 standard; peptide; 21 AA.

AC B10351;

DT 24-NOV-2000 (first entry)

DE Bovine oxytocin secretion promoting peptide SEQ ID NO: 7.

KW: bovine oxytocin secretion promoter; G protein-coupled receptor protein; bovine oxytocin receptor; bovine uterine recovery failure; cow.

KW caesarean section; artificial fertilization; galactostasis; goat; pig;

Pneumonia in children under five years of age

XX
DN
WAC700038704-A-1

XX

XX PF 23-DEC-1999: 99WO-JP07199:

XX
PR 25-DEC-1998: 98JP-0369585.

xx
PA (TAKE) TAKEDA CHEM IND LTD.

Matsutoto H, Kitada C, Hin
PI XX

XX DR WPI: 2000-452298/39:

Physiologically-active Polyp

PT
as drugs for diseases related

XX

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which contains a ligand-peptide or its salt for the G protein-coupled

CC preventing and treating diseases relating to oxytocin secretion e.g.:

uterine recovery failure, caesarean section, stoppage of artificial respiration.

CC medicine for promoting milk production in cow, goat and pig. This

CC promoter.

SO Sequence 21 AA;

卷之三十一

Query Match	100.0%	Score 113;	DB 21;	Leng 21;
Best local Similarity	100.0%	Pred. NO. 8; Le-12;		
W-matches > 0; Conservative	0;	W-mismatches 0;	Indels 0;	Gaps 0;

QY 1 TPDINPAWAGRGRGIRPVGRF 20

Db	1 tpdinpawyagrgrgirpvgrf 20	Qy	1 TPDINPAWYAGRGRGIRPVGRF 20
RESULT 10			
W95193	ID W95193 standard; Peptide: 22 AA.		
AC W95193;			
XX DT 10-MAR-1999 (first entry)			
DE Bovine pituitary-derived ligand polypeptide fragment.			
XX KW pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; DHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; Schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.			
XX OS Bos sp.			
XX PN WO9819295-A1.			
XX PD 05-NOV-1998.			
XX PF 27-APR-1998; 9BWO-JP01923.			
XX PR 28-APR-1997; 97JP-0109974.			
PA (TAKE) TAKEDA CHEM IND LTD.			
XX PI Fukusumi, S., Hinuma, S.			
DR WPI; 1999-009423/01.			
XX PT New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening			
PS Example 19; Page 151; 206pp; English.			
XX CC The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or DHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis; epilepsy; and many others; also to improve post-operative nutritional status and as vasoressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutant are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic polypeptide fragment which is similar to the murine ligand polypeptide.			
XX SQ Sequence 22 AA:			
CC Query Match 100.0%; Score 115; DB 20; Length 22;			
CC Best Local Similarity 100.0%; Pred. No. 8.5e-12;			
CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
CC Qy 1 TPDINPAWYAGRGRGIRPVGRF 20			
CC Db 1 tpdinpawyagrgrgirpvgrf 20			
XX RESULT 12			
XX W31371			
ID W31371 standard; Peptide: 31 AA.			
AC W31371;			
XX DT 06-APR-1998 (first entry)			
XX RESULT 11			
XX DE Bovine oxytocin secretion promoting peptide SEQ ID NO: 8.			
XX ID B10352 standard; peptide: 22 AA.			
XX AC B10352;			
XX DT 24-NOV-2000 (first entry)			
XX DE Bovine oxytocin secretion promoting peptide SEQ ID NO: 8.			
XX KW Bovine; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; cesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.			
KW OS Bos taurus.			
XX PN WO2000038704-A1.			
XX PD 06-JUL-2000.			
XX PF 22-DEC-1999; 99W0-JP07199.			
XX PR 25-DEC-1998; 98JP-0369585.			
PA (TAKE) TAKEDA CHEM IND LTD.			
XX PI Matsumoto H., Kitada C., Hinuma S.			
XX DR WPI: 2000-452298/39.			
XX PT Physiologically active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine -			
XX PS Disclosure; Page 52; 72pp; Japanese.			
XX CC This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion promoter.			
XX SQ Sequence 22 AA:			
CC Query Match 100.0%; Score 115; DB 21; Length 22;			
CC Best Local Similarity 100.0%; Pred. No. 8.5e-12;			
CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
CC Qy 1 TPDINPAWYAGRGRGIRPVGRF 20			
CC Db 1 tpdinpawyagrgrgirpvgrf 20			

Query Match 100.0%; Score 115; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 115; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; gaps 0;

OY 1 TPDINPAWYAGRGRPVWRP 20
 1|||||1|||||1|||||1|||1|||
 Db 12 tpdinpawyagrgrpvgrf 31

RESULT 13
 W97218 ID W97218 standard; peptide; 31 AA.
 XX AC W97218;
 XX DT 06-MAY-1999 (first entry)
 XX

Query Match 100.0%; Score 115; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; gaps 0;

OY 1 TPDINPAWYAGRGRPVWRP 20
 1|||||1|||||1|||||1|||1|||
 Db 12 tpdinpawyagrgrpvgrf 31

RESULT 14
 W87613 ID W87613 standard; Peptide; 31 AA.
 XX AC W87613;
 XX DT 29-MAR-1999 (first entry)
 XX

DE Bovine pituitary-derived ligand polypeptide fragment.
 XX
 KW Bovine pituitary-derived ligand; modulation; prolactin secretion;
 KW G protein-coupled receptor; GPCR; hypogonadism; gynaecost cacosgenesis;
 KW menopausal syndrome; eunuchoid; hypometabolism; lactation;
 KW pituitary adenotaxis; brain tumour; eunuchopathy; autoimmune disease;
 KW prolactinoma, infertility; impotence; amenorrhea; galactorrhea;
 KW acromegaly; Chiari-I-Frommel syndrome; euthyroid; hypometabolism;
 KW Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
 KW contraceptive; placental function; choriocarcinoma; hydatid mole;
 KW irrigation mole; abortion; unthrifly fetus; abnormal saccharometabolism;
 KW abnormal lipidmetabolism; oxytocia.
 XX GS Bos sp.
 XX PN W09859962-A1.
 XX PD 30-DEC-1998.
 XX PR 22-JUN-1998; 98WO-TP02765.
 XX PA 23-JUN-1997; 97JP-0165437.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Fujii R., Fukumumi S., Habata Y., Hinuma S., Hosoya M.;
 XX Kawamata Y., Kitada C.;
 XX DR WPI; 1997-363672/33.
 XX N-P5DB; V02394.

PT Ligand peptide for G protein-coupled receptor - acts by modulating
 function in the central nervous system, pancreas and pituitary gland
 PS Claim 2; Page 160: 258pp; English.

CC This sequence represents a peptide fragment of a novel bovine Pituitary
 CC derived ligand corresponding to amino acid residues 23 to 53 of the
 sequence in WO1368 and is used in an assay to monitor ligand binding to
 CC the G protein-coupled receptor protein. Pharmaceutical compositions
 CC containing this ligand may be used as a pituitary function modulator, a
 CC central nervous system modulator or a pancreatic function modulator. This
 CC ligand could have specific applications as a prophylactic or therapeutic
 CC agent for dementia, depression, hyperkinetic syndrome, disturbance of
 CC consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone
 CC secretory disease, hyper- and polyphagia, hypercholesterolemia,
 CC hyperglycemia, hyperlipidemia, diabetes,
 CC cancer, pancreatic, renal disease, Turner's syndrome, neurosis,
 CC rheumatoid arthritis, spinal injury, transient brain ischaemia,
 CC amyotrophic lateral sclerosis, acute myocardial infarction,
 CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
 CC osteoporosis, asthma, epilepsy, infertility and/or oligogalactia. Assays
 CC can also be developed to screen compounds which are capable of altering
 CC the binding activity of the ligand thus affecting activation of the G
 CC protein-coupled receptor protein.
 XX Sequence 31 AA:

SQ Sequence 31 AA;

Query Match 100.0%; Score 115; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; gaps 0;

OY 1 TPDINPAWYAGRGRPVWRP 20
 1|||||1|||||1|||||1|||1|||
 Db 12 tpdinpawyagrgrpvgrf 31

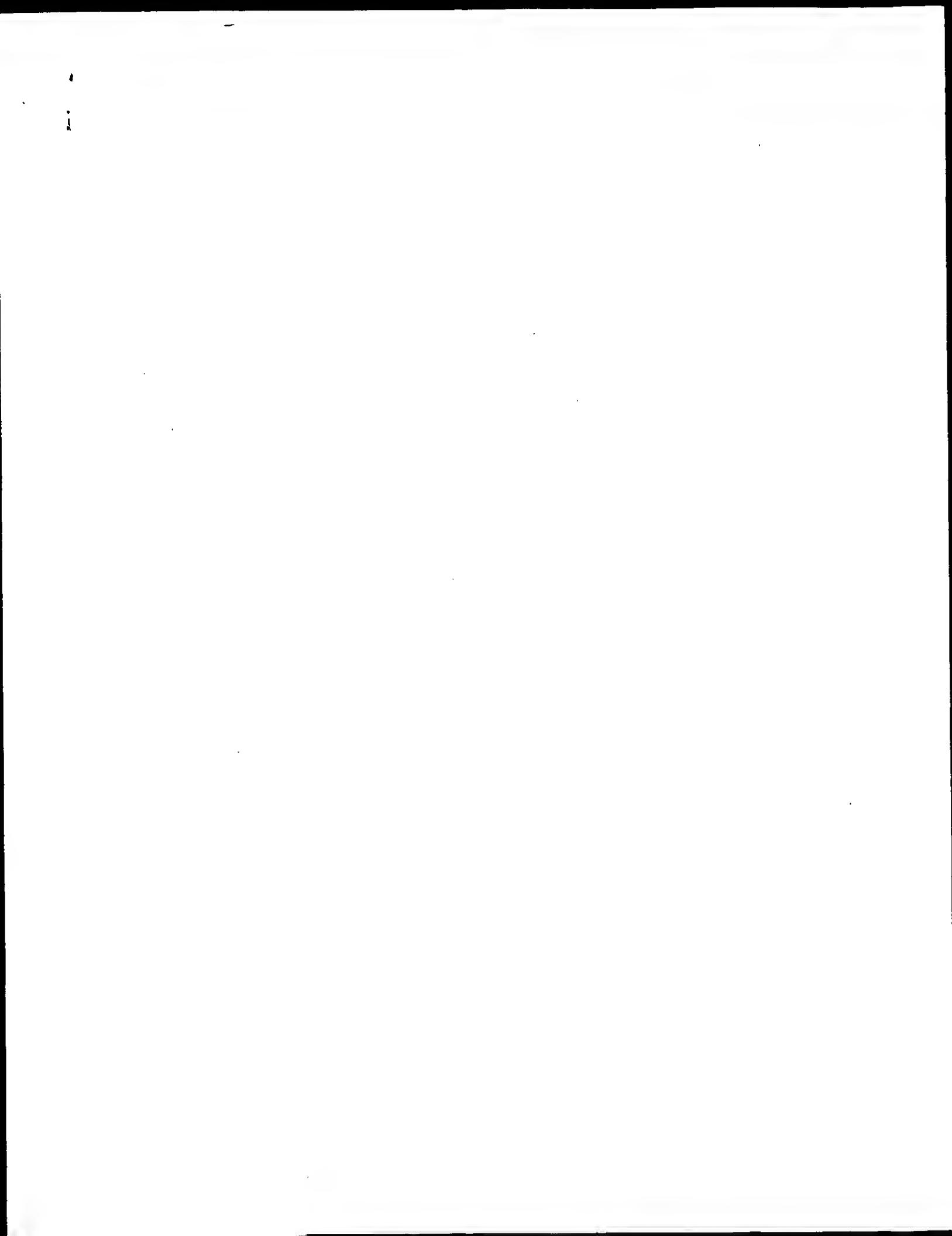
DE	Bovine 19P2 ligand.
KW	19P2 ligand; G protein coupled receptor; pituitary; prolactin releasing peptide; cattle; dementia; breast cancer; therapy.
KW	Bos taurus.
OS	ER987417-A2.
XX	30-DEC-1998.
PF	25-JUN-1998; 98EP-0111725.
XX	PR 27-JUN-1997; 97JP-0172118.
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	PT Moriya T, Nishimura O, Suenaga M, Tanaka Y;
PS	WPI; 1999-047884/05.
XX	PT Producing a 19P2 pituitary G protein receptor ligand - by cleavage of a fusion protein, useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease.
PT	CC This is the amino acid sequence of the bovine pituitary G protein coupled receptor ligand 19P2L. A method suitable for commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see WO93792-93) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanation followed by ammonolysis. 19P2L has prolactin secretion-stimulating and (at high doses) prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including: senile dementia, cerebrovascular dementia, and dementia associated with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's disease, Pick's disease, Huntington's disease), infectious diseases (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or toxicosis (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism, intoxication by drugs, metal and organic compounds), tumourigenic diseases (e.g. brain tumour), traumatic diseases (e.g. chronic subarachnoidal haemorrhage, and other types of dementia, depression, hyperactive child syndrome (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hypo and hypersecretion respectively, including: hyperprolactinaemia, pituitary adenoma, breast cancer, infertility, and autoimmune disease (hypersecretion disorders), and seminal vesicle hypoplasia, osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 19P2 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactagogue in mammalian farm animals.
XX	Sequence 31 AA:
SQ	Query Match 100.0%; Score 115; DB 20; Length 31; Best Local Similarity 100.0%; Pred. No. 1.2e-11; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 TPDINPAWAGRGRIPVGF 20
Db	12 tpdinpawyagrgirgvfrf 31
RESULT	15
ID	W95188
ID	W95188-standard; peptide; 31 AA.
AC	W95188;
XX	10-MAR-1999 (first entry)
DT	Bovine pituitary-derived ligand polypeptide fragment.
XX	Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.
XX	OS Bos sp.
XX	PN WO9849295-A1.
FD	05-NOV-1998.
XX	PR 27-APR-1998; 98WO-JP01923.
XX	PR 28-APR-1997; 97JP-0109974.
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	PI Fukusumi S, Hinuma S;
XX	DR WPI; 1999-009423/01.
XX	PT New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
PS	Example 19; Page 150; 206pp; English.
CC	The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis; epilepsy; and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand polypeptide.
XX	Sequence 31 AA:
SQ	Query Match 100.0%; Score 115; DB 20; Length 31; Best Local Similarity 100.0%; Pred. No. 1.2e-11; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 TPDINPAWAGRGRIPVGF 20
Db	12 tpdinpawyagrgirgvfrf 31

Tue Apr 17 15:46:27 2001

us-09-446-543a-8.ray

Page 9

Job time: 349 sec



us-09-446-543a-8.rai

GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

April 17, 2001, 15:39:47 ; Search time 61.54 Seconds

{without alignments}

6.243 Million cell updates/sec

Title: US-09-446-543a-8
Perfect score: 115
Sequence: 1 TPDINPAWYAGRGIRPVGRF 20

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%,
Maximum Match 100%,
Listing first 45 summaries

Database : Issued_Patents_AA,*

1: /cgnd_6/prodata/2/1aa/5A,COMB.pep:*,
2: /cgnd_6/prodata/2/1aa/5B,COMB.pep:*,
3: /cgnd_6/prodata/2/1aa/6A,COMB.pep:*,
4: /cgnd_6/prodata/2/1aa/6B,COMB.pep:*,
5: /cgnd_6/prodata/2/1aa/PCUS,COMB.pep:*,
6: /cgnd_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	20	3	US-09-105-678A-34
2	115	100.0	21	3	US-09-105-678A-35
3	115	100.0	22	3	US-09-105-678A-36
4	115	100.0	31	3	US-09-105-678A-37
5	115	100.0	31	3	US-09-105-678A-31
6	115	100.0	32	3	US-09-105-678A-32
7	115	100.0	33	3	US-09-105-678A-33
8	111	96.5	20	3	US-09-105-678A-40
9	111	96.5	21	3	US-09-105-678A-41
10	111	96.5	22	3	US-09-105-678A-42
11	111	96.5	31	3	US-09-105-678A-8
12	111	96.5	31	3	US-09-105-678A-37
13	111	96.5	31	4	US-09-105-333-4
14	111	96.5	32	3	US-09-105-678A-38
15	111	96.5	33	3	US-09-105-678A-39
16	109	94.8	19	3	US-09-105-678A-30
17	109	94.8	20	3	US-09-105-678A-46
18	109	94.8	21	3	US-09-105-678A-47
19	109	94.8	22	3	US-09-105-678A-48
20	109	94.8	31	3	US-09-105-678A-9
21	109	94.8	31	3	US-09-105-678A-43
22	109	94.8	32	3	US-09-105-678A-44
23	109	94.8	33	3	US-09-105-678A-45
24	104	90.4	21	3	US-09-105-678A-28
25	104	90.4	29	3	US-08-118-210-71
26	50	43.5	1	US-08-118-210-71	
27	50	43.5	71	APPL Sequence 71, APPL	

ALIGNMENTS

RESULT 1
US-09-105-678A-34
; Sequence 34, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Suenaga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105-678A
; FILING DATE: 26-JUN-1998
; PRIORITY APPLICATION DATA:
; PRIORITY NUMBER: JP 172118/1997
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27-026
; REFERENCE/DOCKET NUMBER: 48466-342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 34:
; LENGTH: 20 amino acids
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-105-678A-34

Query Match 100.0%; Score 115; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPDINPAWAGRG1RPGRF 20
 |||||||
 Sequence 35, Application US/09105678A
 ; Patent No. 6103882

; GENERAL INFORMATION:

; APPLICANT: Suehaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Nishimura, Osamu

; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

RESULT 2

US-09-105-678A-35

; Sequence 35, Application US/09105678A

; Patent No. 6103882

; GENERAL INFORMATION:

; APPLICANT: Suehaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Nishimura, Osamu

; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.3.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09105-678A

; FILING DATE: 26-JUN-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 172118/1997

; FILING DATE: 27-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Conlin, David G.

; REGISTRATION NUMBER: 27,026

; REFERENCE/DOCKET NUMBER: 48466-342

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22 amino acids

; STRANDEDNESS:

; TOPOLOGY: Linear

; MOLECULE TYPE: Peptide

; US-09-105-678A-36

; RESULT 4

US-09-105-678A-7

; Sequence 7, Application US/09105678A

; Patent No. 6103882

; GENERAL INFORMATION:

; APPLICANT: Suehaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Nishimura, Osamu

; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.3.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/09/105,678A

; FILING DATE: 26-JUN-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 172118/1997

; FILING DATE: 27-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Conlin, David G.

RESULT 3

US-09-105-678A-36

; Sequence 36, Application US/09105678A

; Patent No. 6103882

; GENERAL INFORMATION:

; APPLICANT: Suehaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Nishimura, Osamu

; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.3.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/09/105,678A

; FILING DATE: 26-JUN-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 172118/1997

; FILING DATE: 27-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Conlin, David G.

REGISTRATION NUMBER: 27, 026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

; US-09-105-678A-7

Query Match 100.0%; Score 115; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8.5e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-09-105-678A-31
 ; Sequence 31, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ; APPLICANT: Sueenga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109

RESULT 5
 US-09-105-678A-31
 ; Sequence 32, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ; APPLICANT: Sueenga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109

RESULT 6
 US-09-105-678A-32
 ; Sequence 32, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ; APPLICANT: Sueenga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27, 026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

; US-09-105-678A-32

Query Match 100.0%; Score 115; DB 3; Length 32;
 Best Local Similarity 100.0%; Pred. No. 8.8e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 US-09-105-678A-33
 ; Sequence 33, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ; APPLICANT: Sueenga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:

Query Match 100.0%; Score 115; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8.5e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 27-JUN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 26-JUN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: linear

MOLECULE TYPE: peptide

US-09-105-678A-40

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-105-678A-33

Query Match Similarity 100.0%; Score 115; DB 3; Length 33;

Best Local Similarity 100.0%; Pred. No. 9.1e-12; Mismatches 0;

Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 TPDINPAWYAGRGIRPVGFR 20

Db 12 TPDINPAWYAGRGIRPVGFR 31

RESULT 9

Sequence 41, Application US/09105678A

PATENT No. 610882

GENERAL INFORMATION:

APPLICANT: Sueaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: linear

MOLECULE TYPE: peptide

US-09-105-678A-41

Query Match Similarity 95.5%; Score 111; DB 3; Length 21;

Best Local Similarity 95.0%; Pred. No. 2.4e-11;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
 US-09-105678A-42
 ; Sequence 42, Application US/09105678A
 ; Patent No. 610382
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-8

Query Match 96.5%; Score 111; DB 3; Length 22;
 Best Local Similarity 95.0%; Pred. No. 2.5e-11; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
 US-09-105678A-37
 ; Sequence 37, Application US/09105678A
 ; Patent No. 610382
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997

Query Match 96.5%; Score 111; DB 3; Length 31;
 Best Local Similarity 95.0%; Pred. No. 3.be-11; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
 US-09-105-678A-37
 ; Sequence 37, Application US/09105678A
 ; Patent No. 610382
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997

Query Match 96.5%; Score 111; DB 3; Length 22;
 Best Local Similarity 95.0%; Pred. No. 2.5e-11; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
 US-09-105678A-20
 ; Sequence 20, Application US/09105678A
 ; Patent No. 610382
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-52-6440

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: linear

MOLECULE TYPE: peptide

US-09-105-678A-37

Query Match 96.5%; Score 111; DB 3; Length 31;
 Best Local Similarity 95.0%; Pred. No. 3.6e-11;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TPDINPAWYAGRGRGPVGRE 20

Db 12 TPDIINPAWYTGRGRGPVGRE 31

RESULT 13

US-09-172-353-4

Sequence 4, Application US/09172353

Patent No. 619750

GENERAL INFORMATION:

APPLICANT: Stricker-Kongra, Alain

TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS

FILE REFERENCE: 0734/102001

CURRENT APPLICATION NUMBER: US/09/172,353

CURRENT FILING DATE: 1998-10-14

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO: 4

LENGTH: 31

TYPE: PRY

ORGANISM: Mus musculus

US-09-172-353-4

Query Match 96.5%; Score 111; DB 3; Length 32;
 Best Local Similarity 95.0%; Pred. No. 3.7e-11;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TPDINPAWYAGRGRGPVGRE 20

Db 12 TPDIINPAWYTGRGRGPVGRE 31

RESULT 15

US-09-105-678A-39

Sequence 39, Application US/09105678A

Patent No. 610382

GENERAL INFORMATION:

APPLICANT: Moriya, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

RESULT 14

US-09-105-678A-38

Sequence 38, Application US/09105678A

Patent No. 610382

GENERAL INFORMATION:

APPLICANT: Suehaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

RESULT 14

US-09-105-678A-38

Sequence 38, Application US/09105678A

Patent No. 610382

GENERAL INFORMATION:

APPLICANT: Suehaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-52-6440

TELEPHONE: 617-523-6440

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A 39

Query Match 96.5%; score 111; DB 3; Length 33;
Best Local Similarity 95.0%; Pred. No. 3.9e-11; Mismatches 1; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1;

QY	1	TPDINPAWYAGRGIRPVGRF	20
Db	12	TPDINPAWYGRGIRPVGRF	31

Search completed: April 17, 2001, 15:39:47
Job time: 316 sec



Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2001, 15:48:45 ; **search time:** 39.1 seconds
(without alignments)
17.522 Million cell updates/sec

Title: US-09-446-543A-8
Perfect score: 115
Sequence: 1 TPDINPAWAGRGIRPVGRF 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	score	Query Match	Length	DB ID	Description
1	115	100.0	98	1 PRRP_BOVIN	P81264 bos taurus
2	111	96.5	83	1 PRRP_BAT	P81278 rattus norvegicus
3	109	94.8	87	1 PRRP_HUMAN	P81277 homo sapien
4	46	40.0	424	1 SRMB_SALTY	P23832 salmonella
5	46	40.0	424	1 UVRN_METTH	P026543 methanobacter
6	45	39.1	1 EXLI_HUMAN	Q99395 homo sapien	
7	45	39.1	1 UVRN_RAT	P18395 rattus norvegicus	
8	45	39.1	1 UVRN_RHINE	P56199 rhizobium m	
9	44	38.3	1 RE66_GUTH	Q46908 guillardia	
10	44	38.3	1 CICK_CERVI	Q82947 chromatophore	
11	43	37.4	1 YG3D_YEAST	P53381 saccharomyces	
12	43	37.4	1 AIE_HASIN	P44429 haemophilus	
13	43	37.4	1 VAU_ECOLI	P30143 escherichia	
14	43	37.4	1 CP12_CANFA	P56532 canis familiaris	
15	43	37.4	1 UVRN_TERPA	Q83527 treponema p	
16	43	37.4	1 TPDINPAWAGRGIRPVGRF	P90520 dictyostelia	
17	36.5	272	1 TRA2_DROVI	Q02008 drosophila	
18	42	36.5	1 YK2B_MYCLE	Q9x781 mycobacterium	
19	42	36.5	1 VHUJ_ECOLI	P31993 escherichia	
20	42	36.5	1 TRB2_GEOCR	P32925 geotrichum	
21	42	36.5	1 ARP YEAST	P32770 saccharomyces	
22	42	36.5	1 UVRN_MACUT	P94972 mycobacterium	
23	42	36.1	1 TERP_CLOPE	P46306 clostridium	
24	41	35.7	264	1 YSPB_BRCA1	P57436 buchnera ap
25	41	35.7	313	1 VHUJ_ECOLI	P37819 streptomyces
26	41	35.7	322	1 GRP2_MOUSE	P09100 grb2-related
27	41	35.7	330	1 GRP2_HUMAN	Q75791 grb2-related
28	41	35.7	341	1 Y752_MEUTA	Q58172 methanococcus
29	41	35.7	347	1 Y576_MEUTA	Q57995 methanococcus
30	41	35.7	376	1 OPS1_LIMPO	P35360 limulus polyphemus
31	41	35.7	376	1 OPS2_LIMPO	P35361 limulus polyphemus
32	41	35.7	391	1 GAF5_CHICK	P43692 gallus gallus
33	41	35.7	423	1 GCRC_MOUSE	P30731 mus musculus

ALIGNMENTS					
RESULT	1	PRRP_BOVIN	STANDARD;	PRT;	98 AA.
ID	PRRP_BOVIN				
PR	P81264;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	PROLACTIN-RELEASING PEPTIDE PRECURSOR (PRRP) (PROLACTIN-RELEASING HORMONE) [CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20].				
GN					
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.				
OX					
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.				
RC	TISSUE-Brain;				
RX	MEDLINE-#98265781; Published=9807765;				
RA	Hinuma S., Rebata Y., Fujii R., Kawamura Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;				
RT	"A proactin-releasing peptide in the brain"; "A proactin-releasing peptide in the brain";				
RL	Nature 393:272-276(1998); EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.				
CC	-!- FUNCTION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.				
CC	-!- TISSUE-SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its use by non profit Institutions as long as its context is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	DR: EMBL: AB015417; BAM29051; - Hormone; Amidation; Signal; cleavage on pair of basic residues.				
CC	RN: Hormone; Amidation; Signal; cleavage on pair of basic residues.				
FT	SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.				
FT	PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.				
FT	PEPTIDE 33 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).				
FT	MOD_RES 53 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).				
SO	SEQUENCE 98 AA; 10544 MW; 08AC35A13BOFA908 CRC64;				
Query	Match	100.0%; Score 115; DB 1; Length 98;			
Best Local Similarity	100.0%; Pred. No. 7.2e-11; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Ov	1 TPDINPAWAGRGIRPVGRF 20				
Db	34 TPDINPAWAGRGIRPVGRF 53				

RESULT 2
PRRP_RAT STANDARD; PRT; 83 AA.
ID P81278;
AC P81278;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROLACTIN-RELEASING PEPTIDE PRECURSOR (PRRP) (PROLACTIN-RELEASING HORMONE) [CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20].
PRR.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88268781; PubMed=9607765;
RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;
RT "A prolactin-releasing peptide in the brain.";
RL Nature 393:272-275(1998).
CC -!- FUNCTION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.
CC -!- TISSUE SPECIFICITY: MEULLA OBLONGATA AND HYPOTHALAMUS.
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CC -----
DR EMBL; AB01419; BAA29027.1; -.
DR MIM; 602663; -.
KW Hormone; Amidation; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP31.
FT PEPTIDE 34 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
FT MOD_RES 53 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
SQ SEQUENCE 87 AA; 9639 MW; 229A2F3F50C981B CRC64;
CC -----
DR EMBL; AB015418; BAA29056.1; -.
KW Hormone; Amidation; Signal; Cleavage on pair of basic residues.
FT SIGNAL 21 BY SIMILARITY.
FT PEPTIDE 52 PROLACTIN-RELEASING PEPTIDE PRRP31.
FT PEPTIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRRP20.
FT MOD_RES 52 AMIDATION (G-53 PROVIDE AMIDE GROUP).
SQ SEQUENCE 83 AA; 9215 MW; DOC75A264EE4F29 CRC64;
CC -----

Query Match 96.5%; Score 111; DB 1; Length 83;
Best local similarity 95.0%; Pred. No. 2.5e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TPDPINPAWTGGIRPVGRF 20
||||||| ||||| ||||| |||||
Db 33 TPDPINPAWTGGIRPVGRF 52
||||||| ||||| |||||

RESULT 3
PRRP_HUMAN STANDARD; PRT; 87 AA.
ID P81277;
AC P81277;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROLACTIN-RELEASING PEPTIDE PRECURSOR (PRRP) (PROLACTIN-RELEASING HORMONE) [CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20].
PRH.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98268781; PubMed=9607765;
RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;
RT "A prolactin-releasing peptide in the brain.";
RL Nature 393:272-275(1998).
CC -!- FUNCTION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.
CC -!- TISSUE SPECIFICITY: MEULLA OBLONGATA AND HYPOTHALAMUS.
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CC -----
DR EMBL; AB01419; BAA29027.1; -.
DR MIM; 602663; -.
KW Hormone; Amidation; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP31.
FT PEPTIDE 34 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
FT MOD_RES 53 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
SQ SEQUENCE 87 AA; 9639 MW; 229A2F3F50C981B CRC64;
CC -----

Query Match 94.8%; Score 109; DB 1; Length 87;
Best local similarity 95.0%; Pred. No. 5.3e-10; Mismatches 0; Indels 1; Gaps 0;

OY 1 TPDPINPAWTGGIRPVGRF 20
||||||| ||||| |||||
Db 34 TPDPINPAWTGGIRPVGRF 53
||||||| ||||| |||||

RESULT 4
SAMB_SALTY STANDARD; PRT; 424 AA.
ID SAMB_SALTY
AC P23832;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE SAMB PROTEIN.
GN SAMB.
OS Plasmid 60-MDa cryptic.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=91123176; PubMed=1991707;
RA Nohmi T., Hakura A., Nakai Y., Watanabe M., Murayama S.Y., Sofuni T.;
RA "Salmonella typhimurium has two homologous but different umuDC operators: cloning of a new umuDC-like operon (samb) present in a 60-megadalton cryptic plasmid of *S. typhimurium*.";
RL J. Bacteriol. 173:1051-1053(1991).
CC -!- FUNCTION: INVOLVED IN UV PROTECTION AND MUTATION.
CC -!- SIMILARITY: BELONGS TO THE IMPB/MICB/SAMB FAMILY.
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CC -----

FT	CARBONID	269	259	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	676 AA;	74673 MW;	B5E006A8/62E5633 CRC64;
Query Match	Best Local Similarity	39.1%;	Score 45;	DB 1; Length 676;
Matches	9; Conservative	45.0%;	Pred. No. 21;	Mismatches 3; Indels 0; Gaps 0;
QY	1	T P D I N P A W Y A G R G T R P V G R F	20	: : : : : : : : : : : : : : : : :
Db	400	SPQDFFYVLOOGSRPEGRF	419	SEQUENCE
RESULT	7	Rattus norvegicus (Rat).		
UNR_RAT	ID UNR_RAT	STANDARD:	PRT;	798 AA.
AC	P18395;	Score 45;	DB 1;	Length 676;
DR	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
GN	UNR_PROTEIN.			
OS	Rattus norvegicus (Rat).			
OC	Bukar-Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI_TAXID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RX	MEDLINE=90370473; PUBMED=2204029;			
RA	Jeffers M., Faciucci R., Pellicer A.;			
RT	"Characterization of unr, a gene closely linked to N-ras. ";			
RL	Nucleic Acids Res 18:4891-4893(1990).			
CC	-- FUNCTION: RNA-BINDING PROTEIN (BY SIMILARITY).			
CC	-- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: X52311; CAM36549.1; -.			
DR	FIR: S1210; S1210.			
DR	NSP: P15277; IMGC.			
DR	InterPro: IPR02059; -.			
DR	Pfam: PF00313; CSU; 8.			
DR	PROSITE: PS00352; COLD_SHOCK; 4.			
KW	RNA-binding; Repeat; -.			
FT	DOMAIN 26 87 CSD 1.			
FT	DOMAIN 136 179 CSD 2 (INCOMPLETE).			
FT	DOMAIN 186 245 CSD 3.			
FT	DOMAIN 297 337 CSD 4 (INCOMPLETE).			
FT	DOMAIN 349 410 CSD 5.			
FT	DOMAIN 447 507 CSD 6.			
FT	DOMAIN 519 579 CSD 7.			
FT	DOMAIN 610 670 CSD 8.			
FT	DOMAIN 674 735 CSD 9.			
SQ	SEQUENCE 798 AA; 88894 MW; F484B3FAAB095A4 CRC64;			
Query Match	Best Local Similarity	39.1%;	Score 45;	DB 1; Length 973;
Matches	8; Conservative	47.1%;	Pred. No. 24;	Mismatches 2; Indels 18; Gaps 3;
QY	1	T P D I N P A W Y A G R G T R P V G R F	20	: : : : : : : : : : : : : : : : :
Db	717	TPRSNPATYTGAFPIRDWFAAGLPKEAKRGYQP-GRF	752	SEQUENCE
RESULT	9	RK6_GULTH	STANDARD:	PRT; 179 AA.
AC	O46908;			

DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CHLOROPLAST 50S RIBOSOMAL PROTEIN L6.
 GN RPL6.
 OS Guillardia theta (Cryptomonas ph).
 OC Chloroplast.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
 OX NCBI_TaxID=5529;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9128375; PubMed=9137835;
 RA Wang S.-I.; Liu X.-Q.; Douglas S.E.;
 RT "The large ribosomal protein gene organization, sequence and evolutionary implications.";
 RL Biochem. Mol. Biol. Int. 41:1035-1044(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9128221; PubMed=9929392;
 RA Douglas S.E.; Penny S.L.;
 RT "The plastid genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved synteny groups confirm its common ancestry with red algae.";
 RT J. Mol. Evol. 48:236-244(1999).
 CC LOCATED AT THE AMINOACYL-TRNA BINDING SITE OF THE PEPTIDE TRANSFERASE CENTER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 DR EMBL; ABO1811; BAA3742.1; -
 DR InterPro; IPR000345; -
 PROTE; PS00190; CYTOCHROME-C; 4.
 KW Electron transport; Photosynthesis; Reaction center; Heme;
 KW Membrane; Lipoprotein; Duplication; Signal;
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 383 PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT.
 FT LIPID 23 23 N-ACYL DIGLYCERIDE (BY SIMILARITY).
 FT BINDING 107 107 HEME 1 (COVALENT) (BY SIMILARITY).
 FT BINDING 110 110 HEME 1 (COVALENT) (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (HEME AXIAL LIGAND)
 FT BINDING 152 152 HEME 2 (COVALENT) (BY SIMILARITY).
 FT BINDING 155 155 HEME 2 (COVALENT) (BY SIMILARITY).
 FT METAL 156 156 IRON 2 (HEME AXIAL LIGAND)
 FT BINDING 247 247 HEME 3 (COVALENT) (BY SIMILARITY).
 FT BINDING 250 250 HEME 3 (COVALENT) (BY SIMILARITY).
 FT METAL 251 251 IRON 3 (HEME AXIAL LIGAND)
 FT BINDING 307 307 HEME 4 (COVALENT) (BY SIMILARITY).
 FT BINDING 310 310 HEME 4 (COVALENT) (BY SIMILARITY).
 FT METAL 311 311 IRON 4 (HEME AXIAL LIGAND)
 FT
 SQ SEQUENCE 19527 MW; 8B4C0BDB0152AD24 CRC64;

Query Match 38.3%; Score 44; DB 1; Length 179;
 Best Local Similarity 50.0%; Pred. No. 8, 3;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 PAVVAGRGRIPGRF 20
 Db 154 PERYKGKGRIVYGF 168

RESULT 10
 CYC_CHRT
 ID CYC_CHRTV STANDARD; PRM; 383 AA.
 AC 082947;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT PRECURSOR.
 GN PUFC.
 OS Chromatium vinosum.
 OC Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
 OC Allochromatium.
 OX NCBI_TaxID=1049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D;
 RA Corson G.E., Nagashima K.V., Matsuura K., Sakuragi Y., Ruwanthi W.,

Qin H.; Allen R.; Knaff D.B.;
 RA "Primary structure of genes encoding light-harvesting and reaction center proteins from chromatium vinosum";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 RL PURPLE BACTERIA CONTAIN A TIGHTLY BOUND CYTOCHROME MOLECULE WHICH RE-REDUCES THE PROTO OXIDIZED PRIMARY ELECTRON DONOR.
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR (BY SIMILARITY).
 CC -!- PTM: Binds four heme groups per molecule.
 CC -!- SIMILARITY: HIGH, WITH OTHER PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNITS.

RQ
 Qin H.; Allen R.; Knaff D.B.;
 RT "Primary structure of genes encoding light-harvesting and reaction center proteins from chromatium vinosum";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 RL PURPLE BACTERIA CONTAIN A TIGHTLY BOUND CYTOCHROME MOLECULE WHICH RE-REDUCES THE PROTO OXIDIZED PRIMARY ELECTRON DONOR.
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR (BY SIMILARITY).
 CC -!- PTM: Binds four heme groups per molecule.
 CC -!- SIMILARITY: HIGH, WITH OTHER PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNITS.

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RQ
 DR EMBL; ABO1811; BAA3742.1; -
 DR InterPro; IPR000345; -
 PROTE; PS00190; CYTOCHROME-C; 4.
 KW Electron transport; Photosynthesis; Reaction center; Heme;
 KW Membrane; Lipoprotein; Duplication; Signal;
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 383 PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT.
 FT LIPID 23 23 N-ACYL DIGLYCERIDE (BY SIMILARITY).
 FT BINDING 107 107 HEME 1 (COVALENT) (BY SIMILARITY).
 FT BINDING 110 110 HEME 1 (COVALENT) (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (HEME AXIAL LIGAND)
 FT BINDING 152 152 HEME 2 (COVALENT) (BY SIMILARITY).
 FT BINDING 155 155 HEME 2 (COVALENT) (BY SIMILARITY).
 FT METAL 156 156 IRON 2 (HEME AXIAL LIGAND)
 FT BINDING 247 247 HEME 3 (COVALENT) (BY SIMILARITY).
 FT BINDING 250 250 HEME 3 (COVALENT) (BY SIMILARITY).
 FT METAL 251 251 IRON 3 (HEME AXIAL LIGAND)
 FT BINDING 307 307 HEME 4 (COVALENT) (BY SIMILARITY).
 FT BINDING 310 310 HEME 4 (COVALENT) (BY SIMILARITY).
 FT METAL 311 311 IRON 4 (HEME AXIAL LIGAND)
 FT
 SQ SEQUENCE 383 AA; 41522 MW; 96BCD91FFB9AE7E CRC64;

Query Match 38.3%; Score 44; DB 1; Length 383;
 Best Local Similarity 42.1%; Pred. No. 17; Mismatches 8; Indels 0; Gaps 0;
 Matches 8; Conservative 3;

QY 1 PFDINPAVWAGRGRIPGR 19
 Db 263 TPQRATPAWYARHVRDING 281

RESULT 11
 CYC_CHRT
 ID CYC_CHRTV STANDARD; PRM; 241 AA.
 AC 082947;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE NYPOТЕТИЧАЛ 26.1 KDA PROTEIN IN FAS5-CBR2 INTERGENIC REGION.
 GN VGR130W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.

RA van Dyck L., Skala J., de Weerghefesse P., Purnelle B., Talla E.,
 RA Nawrocki A., del Bino S., Goffeau A.;
 RL Submitted (MAY-1995) to the GenBank/DBJ databases.
 CC -I- SIMILARITY: CONAINS 1 SH3 DOMAIN.

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 or send an email to license@isb-sib.ch).

CC DR EMBL: Z72921; CAA9149.1; -.
 DR DR HSSP: P29555; ISEM;
 DR SGD: S0003368; YGR136W.
 DR InterPro: IPR001452; -.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PS00452; SH3DOMAIN.
 DR PROSITE; PS50002; SH3; 1.
 DR KW HYPOTHETICAL PROTEIN; SH3 domain.
 FT DOMAIN 53 112 MW; SH3.
 SQ SEQUENCE 241 AA; 26139 MW; 5F0B1361AF84AA79 CRC64;

Query Match 37.4%; Score 43; DB 1; Length 241;
 Best Local Similarity 41.2%; Pred. No. 16;
 Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 4 INPPAWYAGRGRIPYGRF 20
 Db 86 ISPDPWYRGKSNNKIGIF 102

RESULT 12

ID	ALF_HAEIN	STANDARD;	PRT;	359 AA.
AC	P44429;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, last annotation update)			
DE	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13).			
GN	FBA OR H0524.			
OS	Haemophilus influenzae.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC	Haemophilus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=RD / KW20 / ATCC 51907;			
RX	MEDLINE=95350630; PubMed=7542800;			
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,			
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,			
RA	McKenney K., Sutton G., FitzHugh W., Fields C.A., Gocayne J.D.,			
RA	Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,			
RA	Weldman J.F., Phillips C.A., Spirogs T., Hedblom E., Cotton M.D.,			
RA	Uitterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,			
RA	Fire L.D., Fritchman J.L., Furrmann J.L., Geochagen N.S.M.,			
RA	Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,			
RA	Venter J.C.;			
RT	"whole genome random sequencing and assembly of Haemophilus			
RT	influenzae Rd.;"			
RL	Science 269:496-512(1995).			
CC	-I- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE - GLYCERONE-			
CC	-I- PHOSPHATE + D-GLUCERALDEHYDE 3-PHOSPHATE.			
CC	-I- COFACTOR: ZINC (BY SIMILARITY).			
CC	-I- PATHWAY: SIXTH STEP IN GLYCOLYSIS.			
CC	-I- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-I- SIMILARITY: BELONGS TO CLASS II FRUCTOSE-BISPHOSPHATE ALDOLASE FAMILY.			
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CC	use by non-profit Institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			

CC DR EMBL: U32734; AAC22182.1; -.
 CC DR HSSP: P11604; IDOS.
 CC DR TIGR: H10524; -.
 CC DR InterPro: IPR001071; -.
 CC DR Pfam: PF0116; E_bp_aldolase; 1.
 CC DR PROSITE; PS00602; ALDOLASE_CLASS_II-2; 1.
 CC DR PROSITE; PS00806; ALDOLASE_CLASS_II-2C CRC64;
 CC DR KW Lyase; Glycolysis; Zinc.
 CC FT METAL 108 108 ZINC (BY SIMILARITY).
 CC FT METAL 111 111 ZINC (BY SIMILARITY).
 CC SQ SEQUENCE 359 AA; 39339 MW; LEDPFCDDB69E32C CRC64;

Query Match 37.4%; Score 43; DB 1; Length 359;
 Best Local Similarity 70.0%; Pred. No. 23;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 7 ANVAGAGIRP 16
 Db 67 AFYAGKGKIP 76

RESULT 13

ID	YAJ_ECOLI	STANDARD;	PRT;	476 AA.
AC	P30143;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	HYPOTHECTICAL 51.7 KDa PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8).			
GN	YAJ			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=92334977; PubMed=1630901;			
RA	Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,			
RA	Isono K., Mizobuchi K., Nakata A.,			
RT	"Systematic sequencing of the Escherichia coli genome: analysis of the 0-2.4 min region.";			
RT	Nucleic Acids Res. 20:3305-3308(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=97426617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.,			
RA	"The complete genome sequence of Escherichia coli K-12.";			
RA	Science 277:1453-1474(1997).			
RT	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE (POTENTIAL).			
CC	-I- SIMILARITY: BELONGS TO THE SODIUM-ALANINE SYMPORTER FAMILY (SAF), STRONG, TO H_INFLUENZA HI0183.			
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CC	use by non-profit Institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			

DR EMBL: D10483; -; NOT_ANNOTATED_CDS.
 DR EMBL: AE00111; AAC73118.1; -.
 DR EcoGene; BG1155; yaqJ.
 DR InterPro; IPR001463; -.
 DR PRAM; PF04235; Na,Aia_Symp; 1.
 DR PRINTS; PS00175; NALASLSPORT.
 DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
 KW HYPOTHETICAL PROTEIN; Transmembrane; Inner membrane; Transport;
 KW Symport.
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 141 161 POTENTIAL.
 FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 207 227 POTENTIAL.
 FT TRANSMEM 233 253 POTENTIAL.
 FT TRANSMEM 300 320 POTENTIAL.
 FT TRANSMEM 351 371 POTENTIAL.
 FT TRANSMEM 391 411 POTENTIAL.
 FT TRANSMEM 414 434 POTENTIAL.
 SQ SEQUENCE 476 AA; 51662 MW; 2T6B2E12E126E63 CRC64;

Query Match 37.4%; Score 43; DB 1; Length 476;
 Best Local Similarity 44.8%; Pred. No. 30; Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 3 DIN----PAVAGRCI 14
 AC P56592;
 DB 120 DVNGQFRGGPAPWYMRGL 137

RESULT 14
 ID CP12_CANFA STANDARD; PRT; 511 AA.
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CYTOCHROME P450 1A2 (EC 1.14.14.1) (CYPIA2) (CYTOCHROME P450-
 D2).
 GN CYP1A2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1] SEQUENCE OF 9-511 FROM N.A.
 RP STRAIN-BEAGLE; TISSUE-Liver;
 RX MEDLINE-91042464; PubMed=212230;
 RA Uchida T., Komori M., Kitada M., Kamataki T.;
 RT "Isolation of cDNAs coding for three different forms of liver
 microsomal cytochrome P-450 from polychlorinated biphenyl-treated
 beagle dogs.";
 RL Mol. Pharmacol. 38:644-651(1990).
 RN [2]
 RP SEQUENCE OF 1-16.
 RC STRAIN-BEAGLE; TISSUE-Liver;
 RX MEDLINE-89087526; PubMed=2910310;
 RA Ohta K., Motoya M., Miura T., Kitada M., Kamataki T.;
 RT "A novel form of cytochrome P-450 in beagle dogs. P-450-D3 is a low
 spin form of cytochrome P-450 but with catalytic and structural
 properties similar to P-450d.";
 RL Biochem. Pharmacol. 38:91-96(1989).
 CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
 MONOOXYGENASES IN LIVER MICROSONES. THIS ENZYME IS INVOLVED IN AN
 NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
 OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
 ACIDS, AND XENOBIOCTICS.
 CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
 CC OXIDIZED FLAVOPROTEIN + H(2)O.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
 CC -!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN LIVER.
 CC -!- INDUCTION: BY POLYCHLORINATED BIPHENYL (PCB) IN LIVER AND KIDNEY.

Query Match 37.4%; Score 43; DB 1; Length 511;
 Best Local Similarity 58.3%; Pred. No. 32; Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TPPINPAPWAGR 12
 AC :||| - ||| 132
 DB 121 SPDSCGPWAGR 132

RESULT 15
 ID UVRA_OR_TP0514 STANDARD; PRT; 960 AA.
 DT 08327;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE EXCINUCLEASE ABC SUBUNIT A.
 GN UVRA OR TP0514.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOLS;
 RX MEDLINE=96332770; PubMed=9665876;
 RA Fraser C.M., Morris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwyn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalil B., Richardson D., Howell J.K., Chikambara M., Utterback T.,
 RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Ventre J.C.;
 RP "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete.";
 RL Science 281:375-388(1998).
 CC -!- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
 CC CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
 CC PRODUCING OLIGONUCLES HAVING THE MODIFIED BASE(S). UVRA IS AN APAPSE
 CC AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-
 CC STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
 CC -!- SUBUNIT: CONSISTS OF THREE SUBUNITS: UVRA, UVRB AND UVRc.
 CC -!- SUBUNIT LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SUBCELLULAR (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 CC (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.
 CC
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 CC
 DR EMBL; AE001227; AAC65502.I; -.
 DR InterPro; IPR001128; -.
 DR InterPro; IPR002401; -.
 DR PRAM; PF00067; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PRAM; PR00463; EP4501.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum.
 FT INIT_MER 0
 FT BINDING 453 453 HEME (BY SIMILARITY).
 SQ SEQUENCE 511 AA; 57505 MW; 200904C54FB3CST_CRC64;

Page 8

KW	DNA-binding; zinc-finger.	
FT	NP-BIND	35
FT	NP-BIND	42
FT	NP-BIND	657
FT	NP-BIND	664
FT	2N_FING	270
FT	2N_FING	297
FT	2N_FING	755
FT	2N_FING	782
SEQUENCE	960 AA;	10610 MN;
		32F7824B19F7ABF CRC64;

Search completed: April 17, 2001, 15:48:47
Job time: 535 sec

GenCore version 4.5
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OM Protein - protein search, using sw model

Run on: April 17, 2001, 15:45:51 ; Search time 70.08 Seconds

(without alignments)
(19.613 Million cell updates/sec)

Title: US-09-446-543a-8
perfect score: 115
Sequence: TPDINPAWAGRGIRGVGRF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR:67,*

1:

Pir1;*

2:

Pir2;*

3:

Pir3;*

4:

Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	44.3	430	1	B69009
2	50	43.5	527	2	T33175
3	50	43.5	790	2	T47559
4	48.5	42.2	664	2	F83376
5	46	40.0	333	2	H82852
6	46	40.0	424	2	B38176
7	46	40.0	2	H69157	
8	45.5	39.6	779	2	T49717
9	45	39.1	284	2	F71015
10	45	39.1	757	2	T21969
11	45	39.1	798	2	S11210
12	44	38.3	390	2	G82844
13	43.5	38.3	1670	2	S71551
14	43.5	37.8	506	2	H83396
15	43.5	37.8	506	2	F83142
16	43.5	37.8	1501	2	T45623
17	43	37.4	220	2	C83292
18	43	37.4	241	1	S64445
19	43	37.4	276	1	D70817
20	43	37.4	309	2	T32376
21	43	37.4	359	2	C64074
22	43	37.4	399	2	T30222
23	43	37.4	476	2	G64720
24	43	37.4	503	2	A82193
25	43	37.4	511	2	B37222
26	43	37.4	548	2	T47548
27	43	37.4	950	2	A71315
28	43	37.4	1282	2	T30577
29	43	37.4	1292	2	T31462

RESULT	1
Query	B69009
Match	conserved hypothetical protein MTH1070 - Methanobacterium thermoautotrophicum (strain C; species: Methanobacterium thermoautotrophicum)
Best Local Similarity	44.3%
Score	51
DB	1
Length	430
ID	
Description	conserved hypothetical protein MTH1070 - Methanobacterium thermoautotrophicum (strain C; species: Methanobacterium thermoautotrophicum) #sequence_revision 29-Jan-1999 #text_change 23-Jul-1999
Qy	3 DINPANYAVGRACR 15
Matches	9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db	191 DINPENWAGRACR 203

RESULT	2
Query	T33175
Match	hypothetical protein C24G6.6 - Caenorhabditis elegans
Best Local Similarity	44.3%
Score	51
DB	1
Length	430
ID	
Description	hypothetical protein C24G6.6 - Caenorhabditis elegans #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
Qy	3 DINPANYAVGRACR 15
Matches	9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db	191 DINPENWAGRACR 203

RESULT	2
Query	R;Greco, T.; Bradshaw, H.; Kepler, D.
Match	submitted to the EMBL Data Library, May 1998
Best Local Similarity	44.3%
Score	51
DB	1
Length	430
ID	
Description	submitted to the EMBL Data Library, May 1998
Qy	3 DINPANYAVGRACR 15
Matches	9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db	191 DINPENWAGRACR 203

RESULT	2
Query	A;Description: The sequence of C. elegans cosmid C24G6.
Match	A;Reference number: T221298
Best Local Similarity	44.3%
Score	51
DB	1
Length	430
ID	
Description	A;Description: The sequence of C. elegans cosmid C24G6.
Qy	3 DINPANYAVGRACR 15
Matches	9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db	191 DINPENWAGRACR 203

RESULT	2
Query	A;Cross-references: EMBL:AF067936; PTDN: AAC19213.1; GSPDB: GN00023; CESP:C24G6.6
Match	A;Experimental source: strain Bristol N2; clone C24G6
Best Local Similarity	44.3%
Score	51
DB	1
Length	430
ID	
Description	A;Cross-references: EMBL:AF067936; PTDN: AAC19213.1; GSPDB: GN00023; CESP:C24G6.6
Qy	3 DINPANYAVGRACR 15
Matches	9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db	191 DINPENWAGRACR 203

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PDINPAWYAGRG 13
|::|:|||||
Db 370 PNLVSAWYAGRG 381

RESULT 3

T47959 hypothetical protein F15G16.60 - arabidopsis thaliana

C;Species: Arabidopsis thaliana (house-ear cress)

C;Accession: T47959 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Newes, H.W.; Lemcke, R.; Mayer, K.F.X.; Quettner, A.; Reference number: Z24480

A;Accession: T47959

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-790 <DEH>

A;Cross-references: EMBL:ALI32959

A;Experimental source: cultivar Columbia; BAC clone F15G16

A;Map position: 3 678/2; 698/3; 773/2

A;Note: for a complete list of authors see reference number A82515 below

A;Accession: HB2052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-333 <SIM>

A;Cross-references: GB:AE003860; GB:AE003849; NID:99104830; PIDN:AAF82881.1; GSPPDB:GN

C;Accession: F83376 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

R;Simpson, A.J.G.; Reinach, F.C.; Arriuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrero, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franco, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madelra, H.M.F.; Marino, C.L.; Narques, M.V.; Martins

A;Authors: Martins, E.M.P.; Matsukuna, A.T.; Menck, C.F.M.; Miracca, E.C.; Mikail, C. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Tsukamoto, M.H.; Valiada, H.; van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XPF06B

C;Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 43.5%; Score 50; DB 2; Length 790;

Best Local Similarity 47.4%; Pred. No. 9.2;保守性 9; Mismatches 3; Mismatches 7; Indels 0; Gaps 0;

Db 366 PPHNPRTYGSRSKGPHPGRW 384

RESULT 4

F83376 conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Accession: F83376 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizobuchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Bolger, K.R.; Kas, A.; Labdig, K.; Lim, ; Lory, S.; Olson, M.V.; Titus, J.; Weller, R.O.; Yau, W.; Zeng, Y.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A;Reference number: AB2950; NID:20437337

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-664 <STO>

A;Cross-references: GB:AE004642; GB:AE004091; NID:99948163; PIDN:AAG05539.1; GSPPDB:GN001

A;Experimental source: strain PA01

C;Genetics: PA151

H82852

hydroxybenzoate octaprenyltransferase XFO06B [imported] - Xylella fastidiosa (strain

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C;Accession: H82852

R;anonymous, The Xylella fastidiosa Consortium of the organization for Nucleotide Seq

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; NID:20365717

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: HB2052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-333 <SIM>

A;Cross-references: GB:AE003860; GB:AE003849; NID:99104830; PIDN:AAF82881.1; GSPPDB:GN

C;Accession: F83376 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

R;Nohmi, T.; Hakura, A.; Nakai, Y.; Watanabe, M.; Murayama, S.Y.; Sofuni, T.

J. Bacteriol. 173, 1051-1063, 1991

A;Title: Salmonella typhimurium has two homologous but different umuDc operons: cloni

A;Reference number: A38176; NID:91123176

A;Accession: B38176

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-424 <NOH>

A;Cross-references: GB:D90202; NID:9217087; PIDN:BA14226.1; PID:9217089

A;Experimental source: strain LT2

C;Genetics:

A;Gene: same

C;Function:

A;Description: restores UV mutability; involved in mutagenesis

C;Superfamily: umuC Protein

C;Keywords: DNA repair; induced mutagenesis; SOS mutagenesis

A;Genetics: same

C;Function:

A;Description: restores UV mutability; involved in mutagenesis

C;Superfamily: umuC Protein

C;Keywords: DNA repair; induced mutagenesis

A;Genetics: same

C;Function:

A;Description: restores UV mutability; involved in mutagenesis

C;Superfamily: umuC Protein

C;Keywords: DNA repair; induced mutagenesis

A;Genetics: same

C;Function:

A;Description: restores UV mutability; involved in mutagenesis

C;Superfamily: umuC Protein

C;Keywords: DNA repair; induced mutagenesis

A;Genetics: same

C;Function:

A;Description: restores UV mutability; involved in mutagenesis

C;Superfamily: umuC Protein

C;Keywords: DNA repair; induced mutagenesis

A;Genetics: same

C;Function:

A;Description: restores UV mutability; involved in mutagenesis

C;Superfamily: umuC Protein

C;Keywords: DNA repair; induced mutagenesis

A;Genetics: same

C;Function:

A;Description: restores UV mutability; involved in mutagenesis

C;Superfamily: umuC Protein

C;Keywords: DNA repair; induced mutagenesis

Query Match 40.0%; Score 46; DB 2; Length 424;

Best Local Similarity 53.3%; Pred. No. 20;保守性 8; Mismatches 6; Indels 0; Gaps 0;

Db 478 TPDINPAWYAGRG 16

Query Match 42.2%; Score 48.5; DB 2; Length 664;

Best Local Similarity 62.5%; Pred. No. 13;保守性 10; Mismatches 4; Indels 1; Gaps 1;

Db 478 TPDINPAWYAGRG 16

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length 527;

Best Local Similarity 66.7%; Pred. No. 6.1;保守性 8; Mismatches 2; Indels 0; Gaps 0;

Db 370 PNLVSAWYAGRG 381

Query Match 43.5%; Score 50; DB 2; Length

RESULT 7

Db 384 PGKGIWFGRRGIAPI 398

I : | : | : | : |
excinuclease ABC chain A - Methanobacterium thermoautotrophicum (strain Delta H)

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloudhery, C.; Lee, H.; Dubois, J.; Aldridge, T.;
Riut, D.; Spadtoor, R.; Vicaike, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
N:Contains: excinuclease ABC (EC 3.1.-.-) chain A
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 12-Nov-1999

C:Accession: F169157
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloudhery, C.; Lee, H.; Dubois, J.; Aldridge, T.;
Riut, D.; Spadtoor, R.; Vicaike, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
M.: Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5; 55-76, 1998

A:Title: complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A690000; MUID:98037514

A:Accession: H56157
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-962 <WIL>
A:Experimental source: strain Delta H
A:Genetics:
A:Gene: M1H443

A:Start codon: TGG
A:Keywords: ATP; DNA binding; DNA repair; duplication; hydrolase; P-loop
F:38-45/Region: nucleotide-binding motif A (P-loop)
F:632-656/Region: ATP-binding cassette homology <ABC>
F:649-656/Region: nucleotide-binding motif A (P-loop)

Query Match 40.0%; Score 46; DB 2; Length 962;
Best Local Similarity 37.8%; Pred No. 46; Mismatches 0; Indels 5; Gaps 2;
Matches 14; Conservative 0; Mismatches 5; Indels 18; Gaps 2;

QY 1 TPPINPAWAG-----RGTRPVRF 20
DB 704 TPNSNPATVTSVFTHIRELAQTPEARRKRYRP-GRF 739

RESULT 8

T4917 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
related to BCS1 protein precursor [imported] - Neurospora crassa
N:Alternate names: protein B23L21_300
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T4917
R:Schulte, U.; Alten, V.; Rebeis, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nakamura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T4917
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-767 <WIL>
A:Cross-references: EMBL:768342; PIDN:CAA92775.1; GSPDB:GN00022; CBSP:F38E11.7
A:Experimental source: clone F38E11
C:Genetics:
A:Gene: CESP:F38E11.7
A:MAP position: 4
A:Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1
Query Match 39.1%; Score 45; DB 2; Length 767;
Best Local Similarity 37.5%; Pred No. 52; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDINPANY 9
DB 217 PYIEPFFYALRGLER 234

RESULT 9

T21969 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
hypothetical protein F38E11.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Accession: T21969
R:Matthews, P.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19495
A:Accession: T21969
A:Molecule type: translated from GB/EMBL/DBJ
A:Residues: 1-767 <WIL>
A:Cross-references: EMBL:768342; PIDN:CAA92775.1; GSPDB:GN00022; CBSP:F38E11.7
A:Experimental source: clone F38E11
C:Genetics:
A:Gene: CESP:F38E11.7
A:MAP position: 4
A:Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1
Query Match 39.1%; Score 45; DB 2; Length 767;
Best Local Similarity 37.5%; Pred No. 52; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDINPANY 9
DB 747 PDVKPAWY 754

RESULT 10

T21969 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
hypothetical protein F38E11.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Accession: T21969
R:Matthews, P.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19495
A:Accession: T21969
A:Molecule type: DNA
A:Residues: 1-767 <WIL>
A:Cross-references: EMBL:768342; PIDN:CAA92775.1; GSPDB:GN00022; CBSP:F38E11.7
A:Experimental source: clone F38E11
C:Genetics:
A:Gene: CESP:F38E11.7
A:MAP position: 4
A:Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1
Query Match 39.1%; Score 45; DB 2; Length 767;
Best Local Similarity 37.5%; Pred No. 52; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDINPANY 9
DB 747 PDVKPAWY 754

RESULT 11

S11210 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
probable unr protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Accession: S11210
C:Date: 21-Nov-1993
R:Jeffers, M.; Paciucci, R.; Pellice, A.
Nucleic Acids Res. 18, 4891-4899, 1990
A:Title: Characterization of unr: a gene closely linked to N-ras.
A:Reference number: S11210; MUID:90307473
A:Accession: S11210

A; Molecule type: mRNA	A; Residues: 1-798 <JEE>
A; Cross-references: EMBL:X52311; NID:957454; PIDN:CAA36549.1; PIB:957455	A; Cross-references: EMBL:D29671
C; Keywords: DNA binding	C; Function: <NCI>
	A; Description: as DNA-directed DNA polymerase, catalyzes the polymerization of DNA at
Query Match	A; Description: DNA endonuclease PI-I, catalyzes the hydrolysis of internal phospho
Best Local Similarity 39.1%; Score 45; DB 2; Length 798;	A; Note: DNA endonuclease PI-PSPI
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;	A; Description: as DNA endonuclease PI-II, catalyzes the hydrolysis of internal phospho
Qy 1 TPDINPAWYAGRGRIVY 17	A; Note: DNA endonuclease PI-PSPI
Db 589 TEEANITIYISKVRIL 605	C; Superfamily: DNA-directed DNA polymerase KOD
RESULT 12	C; Keywords: endonuclease; hydrolase; nucleotidyltransferase; protein splicing
G82844 cysteine synthase XP0128 [Imported] - Xylella fastidiosa (strain 9a5c)	F; 1-406; 67-1670/Product: DNA-directed DNA polymerase KOD extein 1 #status predicted
C;Species: Xylella fastidiosa	F; 407-665/Product: DNA endonuclease PI-I (pol KOD Intein 1) #status predicted <XT2>
C;Accession: G82844	F; 767-851/Domain: DNA-directed DNA polymerase KOD extein 2 #status predicted <XT2>
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide sequen	F; 832-1387/Product: DNA endonuclease PI-II (pol KOD Intein 2) #status predicted <XT2>
Nature 405, 151-157, 2000	F; 1388-1670/Domain: DNA-directed DNA polymerase KOD extein 3 #status predicted <XT2>
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.	F; 406-767/Cross-link: peptide (Arg-Ser) #status predicted <XT2>
A;Reference number: A82515; MUID:2036517	F; 851-1388/Cross-link: peptide (Asn-Ser) #status predicted
A;Note: for a complete list of authors see reference number A59328 below	
A;Accession: G82844	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-390 <S10>	
A;Cross-references: GB:AE003866; GB:AE003849; NID:99104906; PIDN:AAE82941.1; GSPDB:GN001	
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acecinio, M.; Alvarenga, R.; P	
Britones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, F	
chado, J.D.; Jungueira, M.L.; Kempfer, E.L.; Kitajima, J.P.; Krueger, J.E.; Kuramae, E.E.; Laigr	
Madeira, A.M.B.N.; Madeira, A.M.F.; Marino, C.L.; Marques, M.V.; Martins, H	
Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.	
submitted to GenBank, June 2000	
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Froim	
o;A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;	
P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmeri, D.M.	
Rodrigues, V.; Rosa, A.J. de M.; de Rosa, V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak	
M.; Tsuchiko, M.H.; Vallada, H.; van Sluys, M.A.; Verjovskii-Almeida, S.; Vettore, A.L.; Z	
A;Reference number: A89328	
A;Contents: annotation	
C;Genetics:	
A;Gene: XF0128	
Query Match	Query Match
Best local Similarity 38.3%; Score 44; DB 2; Length 1670;	Best Local Similarity 38.3%; Score 44; DB 2; Length 1670;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;	Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Qy 5 DINPAWYAGRGRIPVNGRF 20	Qy 3 DINPAWYAGRGRIPVNGRF 20
Db 294 ETIPAWENGENLERYVARY 311	Db 294 ETIPAWENGENLERYVARY 311
RESULT 14	RESULT 14
H83396 probable aldehyde dehydrogenase PA1b64 [Imported] - Pseudomonas aeruginosa (strain PA	H83396 probable aldehyde dehydrogenase PA1b64 [Imported] - Pseudomonas aeruginosa (strain PA
C;Species: Pseudomonas aeruginosa	C;Species: Pseudomonas aeruginosa
C;Accession: H83396	C;Accession: H83396
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;	R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L	adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Lorri, S.; Olson, M.V.	; Lorri, S.; Olson, M.V.
Nature 406, 959-964, 2000	Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa	A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:2043737	A;Reference number: A82950; MUID:2043737
A;Accession: H83396	A;Accession: H83396
A;Status: preliminary	A;Status: preliminary
A;Molecule type: DNA	A;Molecule type: DNA
A;Residues: 1-506 <S10>	A;Residues: 1-506 <S10>
A;Cross-references: GB:AE004625; GB:AE004091; NID:9994793; PIDN:AA05372.1; GSPDB:GN	A;Cross-references: GB:AE004625; GB:AE004091; NID:9994793; PIDN:AA05372.1; GSPDB:GN
C;Keywords: DNA binding	C;Keywords: DNA binding
A;Experimental source: strain PA01	A;Experimental source: strain PA01
A;Genes: PA1b64	A;Genes: PA1b64
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology	C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
Query Match	Query Match
Best Local Similarity 37.9%; Score 43.5; DB 2; Length 506;	Best Local Similarity 37.9%; Score 43.5; DB 2; Length 506;
Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;	Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
Qy 1 TPDINPAWYAGRGRIPVGR 19	Qy 1 TPDINPAWYAGRGRIPVGR 19
Db 436 TRDINRAYRGRGK-AGR 453	Db 436 TRDINRAYRGRGK-AGR 453
RESULT 15	RESULT 15
F83142 probable aldehyde dehydrogenase PA4022 [Imported] - Pseudomonas aeruginosa (strain PA	F83142 probable aldehyde dehydrogenase PA4022 [Imported] - Pseudomonas aeruginosa (strain PA
C;Species: Pseudomonas aeruginosa	C;Species: Pseudomonas aeruginosa
C;Accession: P83142	C;Accession: P83142
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;	R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L	adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Iory, S.; Olson, M.V.	; Iory, S.; Olson, M.V.
Nature 406, 959-964, 2000	Nature 406, 959-964, 2000
A;Title: Cloning and analysis of the DNA polymerase gene from a new hyperthermophil	A;Title: Cloning and analysis of the DNA polymerase gene from a new hyperthermophil
A;Reference number: S71551	A;Reference number: S71551
A;Accession: S71551	A;Accession: S71551
A;Molecule type: DNA	A;Molecule type: DNA

Nature 405, 955-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A;Reference number: A82950; MVID:20437337
A;Accession: F83142
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-506 <STO>
A;Cross-references: GB:AE004619; GB:AE004091; NID:99950214; PIDN:AAG07409.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4022
C;Superfamily: aldehyde dehydrogenase (NAD⁺); aldehyde dehydrogenase homology

Query Match 37.8%; Score 43.5; DB 2; Length 506;
Best Local Similarity 57.9%; Pred. No. 58;
Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy	1	TPDINPAWAGRGRIPVGR	19
		:	:
D _b	436	TRDINRAVRHGRGIK-AGR	453

Search completed: April 17, 2001, 15:45:53
Job time: 601 sec



Om protein - protein search, using sw model
Run on: April 17, 2001, 15:48:03 ; Search time 115.07 Seconds
(without alignments)
20.372 Million cell updates/sec

Title: US-09-446-543A-8
Perfect score: 115
Sequence: 1 TPDINPAWYARGRG1RPVGPF 20

Scoring table: BLOSUM62
Gappen 10.0 , Gapekt 0.5

Searched: 374700 seqs, 117267915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPTRMEL_15;*
- 2: SP_archea;*
- 3: SP_bacteria;*
- 4: SP_fungi;*
- 5: SP_invertebrate;*
- 6: SP_mammal;*
- 7: SP_mhc;*
- 8: SP_organelle;*
- 9: SP_phage;*
- 10: SP_plant;*
- 11: SP_rodent;*
- 12: SP_unclassified;*
- 13: SP_vertebrate;*
- 14: SP_virus;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	90	78.3	117	13	Q9w624 carassius a
2	57	69.6	54	4	Q9w624 homo sapien
3	57	49.6	465	4	Q9w624 homo sapien
4	51	44.3	430	1	Q9w624 methanobacter
5	50	43.5	527	5	Q9w624 caenorhabditis
6	50	43.5	790	10	Q9w624 arabidopsis
7	48	41.7	343	3	Q9w624 coprinus ci
8	46.5	40.4	333	2	Q9w624 streptomyces
9	46	40.0	555	3	Q9w624 xylophaga
10	46	40.0	820	5	Q9w624 aspergillus
11	46	40.0	99NE93		Q9w624 leishmania
12	45.6	39.6	779	3	Q9w624 neurospora
13	45	39.1	284	1	Q9w624 pyrococcus
14	45	39.1	675	2	Q9w624 caenorhabditis
15	44	38.3	153	9	Q9w624 bacteriophaga
16	44	38.3	390	2	Q9w624 xylella fa
17	44	38.3	398	10	Q9w624 osiris arabidopsis
18	44	38.3	419	4	Q9w624 q9w626 homo sapien
19	38.3				Q9w626 oryza sativa
20					Q9w626 oryza sativa

ALIGNMENTS

RESULT	1
ID	Q9w624
AC	Q9w624;
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE	C-RF AMIDE PRECURSOR.
DS	Carassius auratus (Goldfish).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neoperrygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OC	Actinopterygii; Neoperrygii; Teleostei; Euteleostei; Ostariophysi; Cyprinidae; Cyprininae; Carassius.
OC	NCBI_TAXID=7957;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RA	Satake H., Minakata H., Fujimoto M.,
RT	"Carassius Rhamide (C-RF amide).";
RL	Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL	AB020024; BAA6662.1;
DR	SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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Match	Q9w624 homo sapien
Score	90
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PT	117 AA.
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Conservative	5;
Mismatches	2;
Indels	0;
Gaps	0;
Oy	1
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AC	Q9w624
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PT	54 AA.
DB	56
DB	56 SPEIDPFWVWKGVRPIGF 75
Query	Q9w624 carassius a
Match	Q9w624 homo sapien
Score	90
DB	13
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AC	Q9w624
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PT	54 AA.
Matches	13;
Conservative	5;
Mismatches	2;
Indels	0;
Gaps	0;
Oy	1
RESULT	2
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AC	Q9w624
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Conservative	5;
Mismatches	2;
Indels	0;
Gaps	0;
Oy	1
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AC	Q9w624
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Conservative	5;
Mismatches	2;
Indels	0;
Gaps	0;
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Conservative	5;
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Gaps	0;
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Conservative	5;
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Gaps	0;
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Gaps	0;
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AC	Q9w624
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Conservative	5;
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Gaps	0;
Oy	1
RESULT	2
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AC	Q9w624
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Conservative	5;
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Gaps	0;
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AC	Q9w624
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OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RA	Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	RA	Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
NCBI_TAXID=9606;		RA	Harrison D., Hoang L., Keagle P., Lium W., Portier B., Qiu D.,
[1]		RA	Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
SEQUENCE FROM N. A.		RA	Jilani N., Caruso A., Bush D., Safer H., Patwell D., Prabhatar S.,
RA	Lawlor S.;	RA	McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RL	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	RA	Daniels C.J., Mao J.-I., Rice P., Noiling J., Reeve J.N.;
DR	EMBL; AL035608; CAB55682.1; -.	RT	"Complete genome sequence of Methanobacterium thermoautotrophicum
FT	NON_TER 54	RT	delta: functional analysis and comparative genomics.";
SEQUENCE 54 AA; 6110 MW; E2F3C39F79961A9F CRC64;	SQ	RL	J. Bacteriol. 179:7137-7155 (1997).
Query Match 49.6%; Score 57; DB 4; Length 54;	DR	DR	EMBL; AE008977; AB85559.1; -.
Best Local Similarity 56.2%; Pred. No. 0.11;	DR	INTERPRO; IPR002510; -.	
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SQ 18 TPAVMPPTWVAGSGVYP 33	Db	191 DINPEWVAGRGR 203	Best Local Similarity 69.2%; Pred. No. 8; Mismatches 0; Indels 4; Gaps 0;
RESULT 3	RESULT 5	RESULT 5	Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 0;
060687	060687	076383	Query Match 44.3%; Score 51; DB 1; Length 430;
ID PRELIMINARY; PRT; 465 AA.	ID PRELIMINARY; PRT; 527 AA.	ID PRELIMINARY; PRT; 527 AA.	Best Local Similarity 69.2%; Pred. No. 8; Mismatches 0; Indels 4; Gaps 0;
AC 060687;	AC 076383	AC 076383	Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 0;
DT 01-AUG-1998 (TREMBLrel. 07, Created)	DT 01-NOV-1998 (TREMBLrel. 08, Created)	DT 01-NOV-1998 (TREMBLrel. 08, Created)	Query Match 44.3%; Score 51; DB 1; Length 430;
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)	DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)	Best Local Similarity 69.2%; Pred. No. 8; Mismatches 0; Indels 4; Gaps 0;
DE SUSHI-REPETAT PROTEIN.	DE C24G6 6 PROTEIN.	DE C24G6 6 PROTEIN.	Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 0;
GN SRP1.	GN OS	GN OS	Query Match 44.3%; Score 51; DB 1; Length 430;
OS Homo sapiens (Human).	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OS Caenorhabditis elegans.	Best Local Similarity 69.2%; Pred. No. 8; Mismatches 0; Indels 4; Gaps 0;
OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	OC Rhabditida; Peltoderrinae; Caenorhabditis.	Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 0;
DR [1]	DR INTERPRO; IPR000336; -.	DR NCBI_TAXID=6239;	Query Match 44.3%; Score 51; DB 1; Length 430;
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.	DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.	DR NCBI_TAXID=6239;	Best Local Similarity 69.2%; Pred. No. 8; Mismatches 0; Indels 4; Gaps 0;
DR SEQUENCE; 465 AA; 52971 MW; 4D752B187FP3EFB8 CRC54;	DR SEQUENCE; 465 AA; 52971 MW; 4D752B187FP3EFB8 CRC54;	DR NCBI_TAXID=6239;	Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 0;
QY 49.6%; Score 57; DB 4; Length 465;	QY 49.6%; Score 57; DB 4; Length 465;	QY 49.6%; Score 57; DB 4; Length 465;	Query Match 44.3%; Score 51; DB 1; Length 430;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;	Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;	Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;	Best Local Similarity 69.2%; Pred. No. 8; Mismatches 0; Indels 4; Gaps 0;
Db 18 TPAVMPPTWVAGSGVYP 33	Db 18 TPAVMPPTWVAGSGVYP 33	Db 18 TPAVMPPTWVAGSGVYP 33	Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
RESULT 4	RESULT 5	RESULT 5	Query Match 44.3%; Score 51; DB 1; Length 430;
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ID PRELIMINARY; PRT; 430 AA.	ID PRELIMINARY; PRT; 527 AA.	ID PRELIMINARY; PRT; 527 AA.	Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 0;
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GN MTH1070.	GN MTH1070.	GN MTH1070.	Query Match 44.3%; Score 51; DB 1; Length 430;
OS Methanobacterium thermoautotrophicum.	OS Methanobacterium thermoautotrophicum.	OS Methanobacterium thermoautotrophicum.	Best Local Similarity 69.2%; Pred. No. 8; Mismatches 0; Indels 4; Gaps 0;
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;	OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;	OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;	Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 0;
OC Methanobacterium.	OC Methanobacterium.	OC Methanobacterium.	Query Match 44.3%; Score 51; DB 1; Length 430;
NCBI_TAXID=2166;	NCBI_TAXID=2166;	NCBI_TAXID=2166;	Best Local Similarity 69.2%; Pred. No. 8; Mismatches 0; Indels 4; Gaps 0;
[1]			Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 0;
RP SEQUENCE FROM N. A.	RP SEQUENCE FROM N. A.	RP SEQUENCE FROM N. A.	Query Match 44.3%; Score 51; DB 1; Length 430;
RC STRAIN=DETA_H;	RC STRAIN=DETA_H;	RC STRAIN=DETA_H;	Best Local Similarity 69.2%; Pred. No. 8; Mismatches 0; Indels 4; Gaps 0;
RX MEDLINE=918037514; PubMed=9371463;	RX MEDLINE=918037514; PubMed=9371463;	RX MEDLINE=918037514; PubMed=9371463;	Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 0;

Query Match	43.5%	Score 50;	DB 5;	Length 527;
Best Local Similarity	66.7%;	Pred. No. 14;		
Matches	8;	Conservative	2;	Mismatches
			2;	Indels
			0;	Gaps
			0;	
RESULT	6			
ID	09M371	PRELIMINARY;	PRT;	790 AA.
RC	09M371;	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
RP	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	HYPOTHETICAL 87.4 KDA PROTEIN.			
FR	F15G16.60.			
OS	Arabidopsis thaliana (Mouse-ear cress),			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;			
OC	Brassicaceae; Brassicaceae; Arabidopsis.			
NCBI_TaxID	3702;			
[1]	SEQUENCE FROM N.A.			
RA	de Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,			
RA	Mayer K.F.X., Querretier F., Salanoubet M.,			
RA	submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.			
[2]	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RA	Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.			
RL	EMBL; AL132959; CAB71097.1; -.			
RP	SEQUENCE 790 AA; 87375 MW; B222724B75690E30 CRC64;			
RR	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-A3(2);			
RA	Seeger K.J., Harris D.,			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-A3(2);			
RA	Reddenbach M., Kieser H.M., Denapaitre D., Eichner A., Cullum J.,			
RA	Kinashi H., Hopwood D.A.,			
RT	"A set of ordered cosmids and a detailed genetic and physical map for			
RT	the 8 Mb Streptomyces coelicolor A3(2) chromosome."			
RL	MOL Microbiol. 21:77-96 (1996).			
DR	EMBL; AL121746; CAB57411.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 333 AA; 36312 MW; 884FF2861837FD76 CRC64;			
RESULT	7			
ID	074569	PRELIMINARY;	PRT;	343 AA.
RC	074569;	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)			
DE	RAHL.			
GN	Coprinus cinereus (Inky cap fungus),			
OS	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales;			
OC	Coprinaceae; Coprinus.			
NCBI_TaxID	5346;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=OKAYAMA-7;			
RC	MEDLINE=97174112; pubmed=9031132;			
RA	Yeager Stassen N., Loosdron J.M. Jr., Vora G.J., Offenberg H.H.,			
RA	Palmer J.D., Zolan M.E.;			
RT	"Isolation and characterization of rad51 orthologs from Coprinus cinereus and Lycopersicon esculentum, and phylogenetic analysis of eukaryotic rad51 homologs,"			
RT	Cur. Genet. 31:144-157 (1997).			
RL	EMBL; U21905; AAC23703.1; -.			
DR	INTERPRO; IPR000445; -.			
DR	INTERPRO; IPR01553; -.			
DR	PFAM; PF00633; HHH; 1.			
RESULT	8			
ID	09PHT6	PRELIMINARY;	PRT;	333 AA.
AC	09PHT6;	01-OCT-2000 (TREMBLrel. 15, Created)		
DP	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	HYDROXYBENZOATE OCTAPRENYLTRANSFERASE.			
GN	XPF0068.			
OS	Xylella fastidiosa.			
OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; Xylella.			
OC	NCBI_TaxID=2371;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=9A5C;			
RESULT	9			
ID	09PHT6	PRELIMINARY;	PRT;	333 AA.
AC	09PHT6;	01-OCT-2000 (TREMBLrel. 15, Created)		
DP	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	HYDROXYBENZOATE OCTAPRENYLTRANSFERASE.			
GN	XPF0068.			
OS	Xylella fastidiosa.			
OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; Xylella.			
OC	NCBI_TaxID=2371;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=9A5C;			
Query Match	41.7%	Score 48;	DB 3;	Length 343;
Best Local Similarity	50.0%;	Pred. No. 18;		
Matches	9;	Conservative	2;	Mismatches
			2;	Indels
			0;	Gaps
			0;	
QY	1	TPDINPAWAGRGRPVGVG 18		
Db	19	TPWERPAWPWRTEAIGNIARHAAHGIRPTGRW 290		

DR EMBL; AL36172; CAB91698 1; - ; CA7891402DFFBE30 CRC64;
 SQ SEQUENCE 779 AA; 85796 MW; CA7891402DFFBE30 CRC64;
 Query Match 39.6%; Score 45.5; DB 3; Length 779;
 Best local similarity 58.8%; Pred. No. 3e+02; 1; Mismatches 3; Indels 3; Gaps 1;
 Matches 10; Conservative 1; Mismatches 3; Indels 3; Gaps 1;
 Oy 1 PDPINA--WYAGGR 14
 | : ||| ||||| 302
 Db 286 TDYLNFATRYVANTRGL 302

RESULT 13
 050128 PRELIMINARY; PRT; 284 AA.
 ID 050128 DR
 AC 050128 DT
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DE RYPDTTHEICAL 32.3 KDA PROTEIN PH1420.
 GN PH1420.
 OS Pyrococcus horikoshi.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPRINT-OT3;
 RX MEDLINE-9834137; PubMed=9679194;
 RA Kavarrabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamatsu M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kituchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeabacterium, Pyrococcus horikoshi OT3";
 RL DNA Res 5:55-76(1998);
 DR EMBL; AP00006; BAM3-066; 1.
 DR INTERPRO; IPR001066; -.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 284 AA; 32319 MW; 8E0E7BC3711D3815 CRC64;

Query Match 39.1%; Score 45; DB 1; Length 767;
 Best local similarity 50.0%; Pred. No. 42; 1; Mismatches 6; Conservative 1; Indels 0; Gaps 0;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 PDPINPAWYGRGRPVGR 19
 | : ||| ||| : ||| 234
 Db 217 PYIPIPTFYALRGLELIGR 234

RESULT 14
 020170 PRELIMINARY; PRT; 767 AA.
 ID 020170 DR
 AC 020170 DT
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE F38E11.7 PROTEIN.
 GN Caenorhabditis elegans.
 OS Caeorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditida; Palaeodravina; Cadornorhabditis.
 OX NCBL_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matthews P.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Berks M., Coulson A.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Lalancette P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Rooper A., Saunders D., Showman R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sirrot J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans";
 RL Nature 368:32-38(1994).
 DR EMBL; Z68342; CAN2775.1;
 DR INTERPRO; IPR000595; -.
 DR INTERPRO; IPR001622; -.
 DR INTERPRO; IPR002025; -.
 DR PFAM; PF00027; CNMP_binding; 1.
 DR PFAM; PF00914; CNG_membrane; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.
 DR PROSITE; PS50042; CNMP_BINDING_3; 1.
 SQ SEQUENCE 767 AA; 8998 MW; F7ECF69DBBERACF3 CRC64;

Query Match 39.1%; Score 45; DB 5; Length 767;
 Best local similarity 75.0%; Pred. No. 1.2e+02; 1; Mismatches 6; Conservative 1; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 PDPINPAW 9
 | : ||| 747 PDVKPAW 754

RESULT 15
 09T133 PRELIMINARY; PRT; 153 AA.
 ID 09T133 DR
 AC 09T133; DT
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE ENDONUCLEASE.
 GN 3.
 OS Bacteriophage phi-Yeo3-12.
 OC Viruses; dsDNA viruses, no RNA stage; tailed phages; Podoviridae;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PaJunoen M.I., Kiljuner S.J., Skurnik M.;
 RT "Complete genomic sequence of the lytic bacteriophage phi-Yeo3-12 of
 Yersinia enterocolitica serotype O:3";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ251805; CAB65604.1; -.
 KW Endonuclease.
 SQ SEQUENCE 153 AA; 17640 MW; 211571BBDE6C641D CRC64;

Query Match 38.3%; Score 44; DB 9; Length 153;
 Best local similarity 66.7%; Pred. No. 30; 1; Mismatches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 9 YAGRGRGPVGRF 20
 | : ||| : ||| 16
 Db 5 YAARGVRGVGF 16

Search completed: April 17, 2001, 15:48:06
 Job time: 559 sec

Tue Apr 17 15:46:29 2001

us-09-446-543a-8.rspf

us-09-446-543a-47.rpt

134

Best Local Similarity 42.3%; Pred. No. 3.8; Matches 11; Conservative 3; Mismatches 6; Indels 6; Gaps 1; RESULT 3

Query 9 ETRPDINPAWTG----RGIRRV 28
 ||| :|| | :||| :||| :||| :|||
 Db 1175 ETRKTYLNPKVYEGMILKRGYEGVRET 1201

H69157 excinuclease ABC chain A - Methanobacterium thermoautotrophicum (strain Delta H)
 N; Contains: excision endonuclease ABC (EC 3.1.-.) chain A
 N; Alternate names: urvA protein
 C; Species: Methanobacterium thermoautotrophicum
 C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 12-Nov-1999
 C; Accession: H69157
 R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oliu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbaowski, J.; Gibson, R.; Jivani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Moelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional annotation
 A; Reference number: A69000; MUID:98037514
 A; Accession: H69157
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-962 <NTH>
 A; Cross-references: GB:AE000828; GB:AE000666; NID:92621504; PIDN:AA84949.1; PID:9262150
 A; Experimental source: strain Delta H
 C; Genetics:
 A; Gene: MMH443
 A; Start codon: TGG
 C; Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
 C; Keywords: ATP; DNA binding; DNA repair; duplication; hydrolase; P-loop
 F; 38-45; Region: nucleotide-binding motif A (P-loop)
 F; 652-915; Domain: ATP-binding cassette homology <ABC>
 F; 649-656; Region: nucleotide-binding motif A (P-loop)

Query Match 32.2%; Score 56; DB 2; Length 962; Best Local Similarity 42.1%; Pred. No. 5.4; Matches 16; Conservative 0; Mismatches 4; Indels 18; Gaps 2; RESULT 4

Query 11 RTPDINPAWTG-----RGRPVGRF 31
 ||| :||| :||| :||| :||| :|||
 Db 703 RTPRSNPATYTGIVFHIRELFAQTPEARKRCYRP-GRF 739

S11210 probable unr protein - rat
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
 C; Accession: S11210
 R; Jeffries, M.; Paciucci, R.; Pellicer, A.
 R; Nucleic Acids Res. 18, 4891-4899, 1990
 A; Title: Characterization of unr, a gene closely linked to N-ras.
 A; Reference number: S11210; MUID:90370473
 A; Molecule type: mRNA
 A; Residues: 1-798 <JTF>
 A; Cross-references: EMBL:X52311; NID:957454; PIDN:CAA36549.1; PID:957455
 C; Keywords: DNA binding

Query Match 30.5%; Score 53; DB 2; Length 798; Best Local Similarity 43.5%; Pred. No. 12; Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0; RESULT 7

Query 6 HSMEKRTPDINPAWTGGRGRPV 28
 ||| :||| :||| :||| :||| :|||
 Db 583 HSVMGITEANPTISGVIRPL 605

C83070 RESULT 5
 conserves hypothetical protein PA4601 [imported] - Pseudomonas aeruginosa (strain PAO C; Species: Pseudomonas aeruginosa
 C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C; Accession: C83070
 R; Stover, C.C.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adian, S.; Yuan, Y.; Brody, L.I.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A; Reference number: AB2950; MUID:2043733/
 A; Status: preliminary
 A; Accession: C83070
 A; Molecule type: DNA
 A; Residues: 1-1415 <370>
 A; Cross-references: GB:AE04874; GB:AE004091; NID:9950849; PIDN:AAQ07989.1; QSPDB:GN
 A; Experimental source: Strain PA01
 C; Genetics:
 A; Gene: PA4601

Query Match 30.5%; Score 53; DB 2; Length 1415; Best Local Similarity 37.5%; Pred. No. 22; Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0; RESULT 6

Query 1 SRAOHSMETTPDINPAWYGRF 24
 ||| :||| :||| :||| :|||
 Db 330 AQAROHHLGLGLDPLEPGWLJDAG 353

A82329 Query Match 30.5%; Score 53; DB 2; Length 1415; Best Local Similarity 37.5%; Pred. No. 22; Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0; RESULT 6

excinuclease ABC chain A VC0394 [imported] - Vibrio cholerae (group O1 strain N16961 C; Species: Vibrio cholerae
 C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
 C; Accession: A82329
 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. J.; Charlsnia, D.; Brzustowski, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A; Title: DNA sequence of both chromosomes of the cholera pathogen vibrio cholerae.
 A; Reference number: AB2035; MUID:20406833
 A; Accession: A82329
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-940 <HEI>
 A; Cross-references: GB:AE004127; GB:AE003852; NID:99654808; PIDN:AAF93567.1; QSPDB:GN
 A; Experimental source: serogroup O1; strain N16961; biotype El Tor
 C; Genetics:
 A; Gene: VC0394
 A; Map position: 1
 C; Superfamily: excinuclease ABC chain A; ATP-binding cassette homology

Query Match 29.9%; Score 52; DB 2; Length 940; Best Local Similarity 39.5%; Pred. No. 20; Matches 15; Conservative 1; Mismatches 4; Indels 18; Gaps 2; RESULT 7

Query 11 RTPDINPAWTG-----RGRPVGRF 31
 ||| :||| :||| :||| :|||
 Db 694 RTPRSNPATYTGIFTPIRELAGTOESRSRGVQ-GRF 730

R70619 Query Match 29.9%; Score 52; DB 2; Length 940; Best Local Similarity 39.5%; Pred. No. 20; Matches 15; Conservative 1; Mismatches 4; Indels 18; Gaps 2; RESULT 7

excinuclease ABC chain A - Mycobacterium tuberculosis (strain H37RV)
 N; Contains: excision endonuclease ABC (EC 3.1.-.) chain A
 C; Species: Mycobacterium tuberculosis
 C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C; Accession: A70619
 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, R.; Tait, A.; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A; Reference number: A70500; MUID:98295987
 A; Accession: A70500
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-972 <COL>
 A; Cross-references: GB:Z25982; GB:AU123456; NID:9326176; PIDN:CA06633.1; PID:91838989
 A; Experimental source: strain H37Rv
 C; Genetics:
 A; Gene: uvrA
 C; Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
 C; Keywords: ATP; DNA binding; DNA repair; hydrolase
 F; 32-33/Region: nucleotide-binding motif A (P-loop)
 F; 637-920/Domain: ATP-binding cassette homology <ABC>
 F; 654-661/Region: nucleotide-binding motif A (P-loop)

Query Match 29.9%; Score 52; DB 2; Length 972;
 Best Local Similarity 39.5%; Pred. No. 21; Matches 15; Conservative 1; Mismatches 4; Indels 18; Gaps 2;
 QY 11 R^WP^DI^NA^PW^TG-----RG^R 31
 ||| |||| ||| - | : || : ||| 744
 Db 708 R^WR^SN^PA^TY^GV^FK^RT^LF^AT^EA^KV^RQ^YP⁻G^RF 744

RESULT 8
 A83193 Sun/nucleolar protein family protein vc1502 [imported] - *Vibrio cholerae* (group O1 strain C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
 C; Accession: A82193 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gruen, M.L.; Dodson, R.J.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
 A; Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*. A; Reference number: A82035; MUID:20406833 A; Accession: A82193 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1503 <HEI> A; Cross-references: GB:AE004228; GB:AE003852; NID:99655997; PIDN:AAF94657.1; GSPDB:GN001 C; Genetics:
 A; Gene: vc1502 A; Map position: 1

Query Match 29.6%; Score 51.5; DB 2; Length 503;
 Best Local Similarity 36.7%; Pred. No. 12; Matches 11; Conservative 5; Mismatches 13; Indels 1; Gaps 1;
 QY 1 1 S^RA^QH^SM^TR^PI^NA^PW^TG^RG^RP^VG^R 30
 ||| : ||| - | : || : ||| : ||| 463
 Db 435 S^RS^AH^SV^EL^DT^QA^R-E^HM^GR^OV^RP^EQ 463

RESULT 9
 T21075 hypothetical protein F19H6.1 - *Caenorhabditis elegans* C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
 C; Accession: T21075; T2124 R; McMurray, A.
 submitted to the EMBL Data Library, August 1995
 A; Reference number: Z19686 A; Accession: T21075 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Cross-references: experimental source: strain H37Rv
 C; Genetics:
 A; Gene: uvrA
 C; Function: has ATPase and DNA binding activity; involved in DNA repair
 A; Description: has ATPase and DNA binding activity; involved in DNA repair
 C; Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
 C; Keywords: ATP; DNA binding; DNA repair; duplication; hydrolase; P-loop
 F; 31-38/Region: nucleotide-binding motif A (P-loop)
 F; 623-907/Domain: ATP-binding cassette homology <ABC>
 F; 640-647/Region: nucleotide-binding motif A (P-loop)

Query Match 29.3%; Score 51; DB 2; Length 943;
 Best Local Similarity 39.5%; Pred. No. 28; Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;
 QY 3 A^HQ^HS^ME^TR^PD^IN^A--W^TG^RG^RP^VG 29
 ||| ||| ||| : ||| : ||| : ||| 139
 Db 139 A^HM^SK^RI^MR^DI^KP^NV^IT^GN^GI^VK^LG 167

RESULT 10
 D64057 excinuclease ABC chain A - *Haemophilus influenzae*
 N; Alternative names: uvrA protein
 N; Contains: excision endonuclease ABC (EC 3.1.-.-) chain A
 C; Species: *Haemophilus influenzae*
 C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 12-Nov-1999
 C; Accession: D64057; JCS157 R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.J.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandau, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
 A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, B.O.; Venter A; Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd. A; Reference number: A86400; MUID:9530630 A; Accession: D64057 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-943 <TRG>
 A; Cross-references: GB:032711; GB:142023; NID:91573214; PIDN:AC21915.1; PID:91573215 A; Experimental source: strain Rd KW20 R; de la Morena, M.I.; Hendrixson, D.R.; St Geme III, J.W. Gene 177, 23-28, 1996
 A; Title: Isolation and characterization of the *Haemophilus influenzae* uvrA gene. A; Reference number: JCS157; MUID:97080495 A; Accession: JCS157 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-162; L, 164-235, 'D', 237-424, 'K', 426-462, 'M', 464-513, 'Q', 515-660, 'T', 662 A; Cross-references: GB:033877; NID:91144488; PIDN:AC44592.1; PID:9144489 A; Experimental source: strain NIB7 C; Genetics:
 A; Gene: uvrA
 C; Function: has ATPase and DNA binding activity; involved in DNA repair
 A; Description: has ATPase and DNA binding activity; involved in DNA repair
 C; Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
 C; Keywords: ATP; DNA binding; DNA repair; duplication; hydrolase; P-loop
 F; 31-38/Region: nucleotide-binding motif A (P-loop)
 F; 623-907/Domain: ATP-binding cassette homology <ABC>
 F; 640-647/Region: nucleotide-binding motif A (P-loop)

Matches 15; Conservative 0; Mismatches 5; Indels 18; Gaps 2;
 Qy 11 RPPDINPAWYG-----RGIRPGRF 31
 ||| ||| ||| ||| |||
 Db 695 RPPRSNPATVIGLFTPIRELFGAGVPEARARGYNP-GRF 731
 ||| ||| ||| |||
 RESULT 14
 S67150 hypothetical protein YDR253W - yeast (Saccharomyces cerevisiae)
 N;Alternate names: hypothetical protein 05315
 C;Species: Saccharomyces cerevisiae
 C;Accession: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Nov-1999
 R;Jauniaux, J.C.; Poirey, R.
 submitted to the Protein Sequence Database, July 1996
 A;Reference number: S67143
 A;Accession: S67150
 A;Molecule type: DNA
 A;Residues: 1-176 <BAU>
 A;Cross-references: EMBL:MG2092; NTB:9172615; PIDN:AAA35051.1; PID:9172616
 R;Dietrich, F.S.
 A;Description: The sequence of 5. cerevisiae cosmids 9481, 9509, 9926, 9461, and Lamb
 A;Reference number: 569665
 A;Accession: S69672
 A;Molecule type: DNA
 A;Residues: 1-482 <DE>
 A;Cross-references: EMBL:U32274; NTB:927313; PIDN:AAB64830.1; PID:927321; GSDB:GNO
 C;Genetics:
 A;Gene: SGD:RVS167; MIPS:YDR388w
 A;Cross-references: SGD:SD002796; MIPS:YDR388w
 A;Name position: 4R
 C;Superfamily: RVS167 protein; RVS161 protein homology; SH3 homology
 C;Keywords: transmembrane protein
 F:4-270(Domain: RVS161 protein homology <RVS>
 F:292-427/Region: alanine/glycine/proline-rich
 F:428-477/Domain: SH3 homology <SH3>

Query Match 29.0%; Score 50.5; DB 2; Length 176;
 Best Local Similarity 31.2%; Pred. No. 5.4; Mismatches 15; Indels 3; Gaps 1;
 Matches 10; Conservative 4; Mismatches 15; Indels 3; Gaps 1;
 Qy 1 SRAHQHSMETRTP---DINPAWYTGRGRIPVG 29
 ||| ||| : | ; | : | | |
 Db 120 SECHQHNWVIVUPAVDDLTQWELIAHGFEOVG 151

RESULT 12

T47548 hypothetical protein F8J2.80 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C;Accession: T47548
 R;Nyakatura, G.; Furtmann, B.; Dauner, D.; Starr, R.; Holland, R.; Weichselgarther, M.;
 Mayer, K.F.X.; submitted to the Protein Sequence Database, April 2000
 A;Reference number: 224458
 A;Accession: T47548
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-154 B <NTA>
 A;Cross References: EMBL:AU132969
 A;Experimental source: cultivar Columbia; BAC clone F8J2
 C;Genetics:
 A;Gene position: 3
 A;Nap position: 3
 A;Introns: 78/1; 143/1; 242/2; 377/3; 428/2; 447/3; 470/3; 502/3; 532/3
 A;Note: F8J2.80

Query Match 29.0%; Score 50.5; DB 2; Length 548;
 Best Local Similarity 35.5%; Pred. No. 18; Mismatches 10; Indels 7; Gaps 1;
 Matches 11; Conservative 3; Mismatches 10; Indels 7; Gaps 1;

RESULT 14

RVS167 protein - yeast (Saccharomyces cerevisiae)
 N;Alternate names: protein YDR388w
 C;Species: Saccharomyces cerevisiae
 C;Accession: 31-Mar-1992 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Nau, B.; Shao, Y.
 Science 277: 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A04720; MOLD:97426617
 A;Accession: A65214
 A;Cross-references: R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Nau, B.; Shao, Y.
 Science 277: 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A04720; MOLD:97426617
 A;Accession: A65214
 A;Status: preliminary: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-940 <BLA>
 A;Cross-references: GB:AE00479; GB:U00096; NID:92367340; PIDN:AC77028.1; PID:923673
 A;Experimental source: strain K-12, substrain MG1655

RESULT 13

S4087 RVS167 protein - yeast (Saccharomyces cerevisiae)

C;Species: Saccharomyces cerevisiae
 C;Accession: 31-Mar-1992 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000

C;Comment: This protein is an ATP-dependent DNA repair enzyme that catalyzes the excision reaction of UV-damaged e, an ATP-binding cassette homology domain containing nucleotide-binding motif A (P-loop) protein.

A;Map position: 92 min

C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology domain containing nucleotide-binding motif A (P-loop)

C;Keywords: ATP; DNA binding; DNA repair; duplication; hydrolase; P-loop

F;31-38/Region: nucleotide-binding motif A (P-loop)

F;623-907/Region: ATP-binding cassette homology <ABC>

F;640-647/Region: nucleotide-binding motif A (P-loop)

Query Match 28.7%; Score 50; DB 1; Length 940;

Qy	11	RTPDINPAWYG-----RGIRGVGRF	31
Db	695	RTPRSNPATYTGVETPVRELFAGVPESRARGYTP-GRF	731

RESULT 15

D11645 excinuclease ABC chain A (uvrA) RP835 - Rickettsia prowazekii

Ni: Contains: excision endonuclease ABC (EC 3.1.-.-) chain A

C;Species: Rickettsia prowazekii

C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000

C;Accession: D11645

R;Andersson, S.G.E.; Zamorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U; Nature 396, 133-140, 1998

A;Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.

A;Reference number: A71630; NUID:99039499

A;Accession: D11645

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-953 <AND>

A;Cross-references: GB:AJ235273; GB:AJ235269; NIDB:93861237; PIDN:CAA15260.1; PID:9386136

A;Experimental source: strain Madrid E

C;Genetics:

A;Gene: uvrA; RP835

C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology domain containing nucleotide-binding motif A (P-loop)

C;Keywords: ATP; DNA binding; DNA repair; hydrolysis

F;33-40/Region: nucleotide-binding motif A (P-loop)

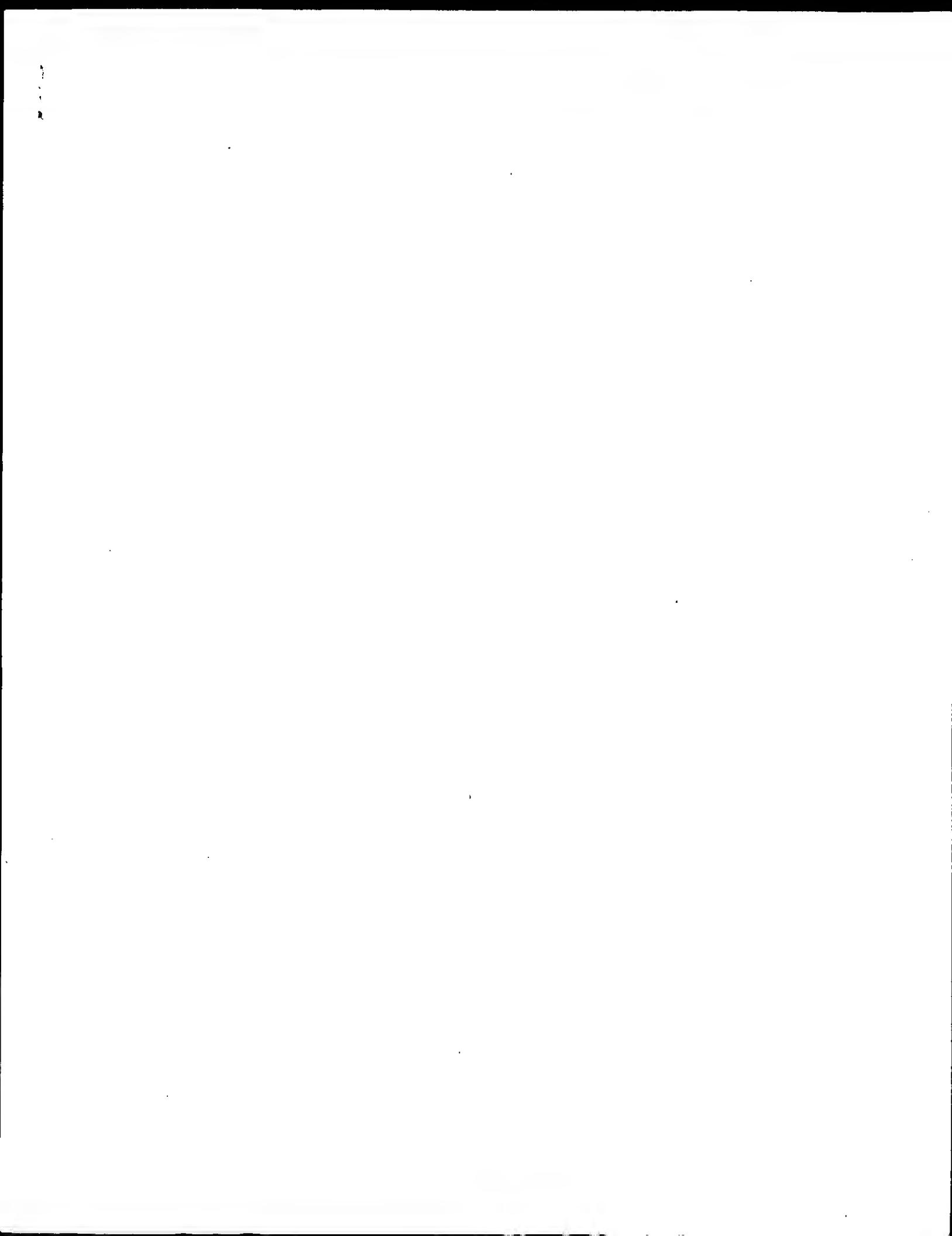
F;635-919/Region: ATP-binding cassette homology <ABC>

F;652-659/Region: nucleotide-binding motif A (P-loop)

Query Match 28.7%; Score 50; DB 2; Length 953;

Qy	11	RTPDINPAWYG-----RGIRGVGRF	31
Db	707	RTPRSNPATYTGVETPVRELFAGVPESRARGYTP-GRF	743

Search completed: April 17, 2001, 15:45:54
Job time: 602 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2001, 15:48:06 ; Search time 115.07 seconds

(without alignments)
31.576 Million cell updates/secUS-09-446-543a-47
174 SRAHQSMETRIPDINPAWYRGIRPVGRF 31

Scoring table: BLOSUM62

Gap0 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTRIMBL_15;*
- 2: sp_archaea;*
- 3: sp_bacteria;*
- 4: sp_fungi;*
- 5: sp_invertebrate;*
- 6: sp_mammal;*
- 7: sp_mhc;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp_rodent;*
- 12: sp_unclassified;*
- 13: sp_vertebrate;*
- 14: sp_virus;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	107	61.5	117	13	Q9W624 carassis a
2	68	39.1	692	2	Q918J6 rhodospirill
3	61	35.1	1236	2	Q9JPA4 rhodococcus
4	58	33.3	1292	2	Q9ZGE5 heliobacillus
5	56	32.2	428	6	Q97859 bos taurus
6	53	30.5	304	4	Q9UJF9 homo sapien
7	53	223	2	Q9W605	085605 prevotella
8	53	30.5	465	4	Q60087 homosapien
9	52	29.9	503	10	Q91SC6
10	52	29.9	940	2	Q9KRW5
11	51	29.6	503	2	Q9KRZ1
12	51	29.3	294	5	Q91530 caenorhabdit
13	51	29.3	428	4	Q95049 homosapien
14	51	29.3	629	4	Q9NQEL homosapien
15	50.5	29.0	176	3	Q9B689 saccharomyces
16	50.5	29.0	333	2	Q9RJ10 streptomyces
17	50.5	29.0	414	2	Q33480 propionibacter
18	50.5	29.0	538	4	Q9Y4C9 homosapien
19	50.5	29.0	548	10	Q9LFA0 arabidopsis

RESULT	1	PRELIMINARY:	PRT;	117 AA.
ID	Q9W624			
AC	Q9W624;			
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	01-NOW-1999	(TREMBLrel. 12, Last annotation update)		
DE	C-RF AMIDE PRECURSOR.			
OS	Carassius auratus (Goldfish).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Carassius.			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cyprinidae; Cyprininae; Carassius.			
OX	NCBITAXID=7957;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RA	Satake H., Minakata H., Fujimoto M.;			
RP	"Carassius RFamide (C-RF amide)." ;			
RL	Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AB02024; BAA7662; 1; -.			
SQ	SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;			
	Query Match	61.5%; Score 107; DB 13;	Length 117;	
	Best Local Similarity	57.7%; pred. No. 4.5e-08;		
	Matches	15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;		
Qy	6 HSMETRIPDINPAWYRGIRPVGRF 31			
Db	50 INVDRRSPEIDPFWYGRGVPRGF 75			
	RESULT	2		
ID	Q9L8J6	PRELIMINARY;	PRT;	692 AA.
AC	Q9L8J6;			
DT	01-OCT-2000 (TREMBLrel. 15, created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, last annotation update)			
DE	BCHH (FRAGMENT).			
GN	GN			
	Rhodospirillum rubrum.			

OC	Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;	DR	EMBL: AB034704; BAA94057.1; -.
OC	Rhodospirillum.	KW	Transferase.
RN	"[1]"	SEQUENCE	1236 AA; 134729 MW; 84051C045638520C CRC64;
RP	SEQUENCE FROM N.A.		
RC	STRAIN="R5;"		
RX	Medline=20138142; PubMed=10671438;		
RA	Cheng Y.S., Brantner C.A., Tsapin A., Collins M.L.P.;		
RT	"Role of the H protein in assembly of the photochemical reaction center and intracytoplasmic membrane in Rhodospirillum rubrum.";		
RT	J. Bacteriol. 182:1200-1207 (2000).		
RL	EMBL; AF202319; AAC37521; -.		
DR	NON-TER 1		
SQ	SEQUENCE 692 AA; 75453 MW; 96430AE93BF35680 CRC64;		
RESULT	3	RESULT	4
Q9JPA4	PRELIMINARY:	Q9ZGE5	PRELIMINARY:
ID	Q9JPA4	ID	Q9ZGE5
AC	01-OCT-2000 (TREMBLrel. 15, created)	AC	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	MC PROTOPORPHYRIN METHYL TRANSFERASE.	DE	MG CHELATASE SUBUNIT H BCHH.
GN	BCHH.	GN	BCHH.
OS	Rhodococcus gelatinosus (Rhodopseudomonas gelatinosa).	OS	Hellobacillus mobilis.
OC	Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;	OC	Bacteria; Firmicutes; Bacillus/Clostridium group;
OC	Rubrivivax.	OC	Hellobacillus group; Hellobacillus.
OX	NCBI_TaxID=28068;	OX	NCBI_TaxID=28064;
RN	[1]	RN	
RP	SEQUENCE FROM N.A.	RP	
RC	STRAIN="IL144;"	RA	XI LONG J., Inoue K., Bauer C.E.;
RA	Nagashima K.V., Shimada K., Matsuura K.;	RT	"Tracking molecular evolution of photosynthesis by characterization of a major photosynthesis gene cluster from Hellobacillus mobilis.";
RP	"Phylogenetic analysis of photosynthetic genes of Rhodococcus gelatinosus: possibility of horizontal gene transfer in purple bacteria.";	RT	Proc. Natl. Acad. Sci. U.S.A. 95:14551-14561(1998).
RT	Photosyn. Res. 36:185-191(1993).	DR	EMBL; AF080002; AAC84033.1; -.
RL	[2]	SQ	SEQUENCE 1292 AA; 144853 MW; 323AA0517B07448D CRC64;
RN	SEQUENCE FROM N.A.	RESULT	5
RC	STRAIN="IL144;"	Q97859	Query Match
RX	MEDLINE=99132007; PubMed=8300574;	ID	33.3%; Score 58; DB 2; Length 1292;
RA	Nagashima K.V., Matsuura K., Ohyama S., Shimada K.;	AC	Best Local Similarity 42.3%; Pred. No. 6.8; Mismatches 6; Indels 6; Gaps 1;
RT	"Primary structure and transcription of genes encoding B870 and photosynthetic reaction center apoproteins from Rubrivivax	DT	01-MAY-1999 (TREMBLrel. 10, Created)
RT	"gelatinosus.";	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
RT	J. Biol. Chem. 269:2477-2484(1994).	DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
RL	[3]	DE	GANGLIOSIDE SIALIDASE.
RN	SEQUENCE FROM N.A.	OS	Bos taurus (Bovine).
RC	STRAIN="IL144;"	OC	Elkarlota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA	Igarashi N., Shimada K., Matsuura K., Nagashima K.V.;	OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
RT	"PHOTOSYNTHETIC GENE CLUSTER IN PURPLE BACTERIUM, RUBRIVIVAX GELATINOSUS.", (In) Garcia G. (eds);	OC	Bovidae; Bovinae; Bos.
RT	Photosynthesis. Mechanisms and Effects IV:2889-2892;	OX	NCBI_TaxID=9913;
RL	RL Kluwer Academic Publishing (1998).	RN	[1]
RN	[4]	RP	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RC	TISSUE-BRAIN;
RC	STRAIN="IL144;"	RX	MEDLINE=99143165; PubMed=9988745;
RT	Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K., Parot P., Vermeglio A.;	RA	Miyagi T., Wada T., Iwamatsu A., Hata K., Yoshioka Y., Tokuyama S., Sawada M.;
RT	"Dark aerobic growth conditions induce the synthesis of a high midpoint potential cytochrome c8 in the photosynthetic bacterium Rubrivivax gelatinosus";	RA	"Molecular cloning and characterization of a plasma membrane-associated sialidase specific for gangliosides.";
RT	Rubrivivax gelatinosus";	RT	J. Biol. Chem. 274:5045-5011(1999).
RL	"Biochemistry 0:0-0(1999)."	DR	EMBL; AB00184; BAA15071.1; -.
DR	INTERPRO: IPR002860; -.	DR	PFAM: PF02012; BNR; 3.
SQ	SEQUENCE 428 AA; 47916 MW; 418B34F3245ABF21 CRC64;	DR	PFAM: PF02012; BNR; 3.

Query Match 32.2%; Score 56; DB 6; Length 428;
 Best Local Similarity 37.0%; Pred. No. 4.1;
 Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

RESULT 6

QYUJF9 PRELIMINARY; PRT: 54 AA.

ID QYUJF9; PRELIMINARY; PRT: 54 AA.

AC QYUJF9; PRELIMINARY; PRT: 54 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE DJ47937.3. (SUSHI-REPEAT PROTEIN (SRPUL)) (FRAGMENT).

GN [1]

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

RN RN

RP SOURCE FROM N.A.

RA Lawlor S.; Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL; AL035608; CAB55682.1; -.

DR NON_TER 54 54

FT SEQUENCE 54 AA; 6110 MW; EZP3C39F7B961A9F CRC64;

Query Match 30.5%; Score 53; DB 4; Length 54;
 Best Local Similarity 50.0%; Pred. No. 1.2;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 12 TPDINPAWVGRGIRP 27

Db 18 TPAVIPTWAGSGVYP 33

RESULT 7

QYUJF605 PRELIMINARY; PRT: 223 AA.

ID QYUJF605 PRELIMINARY; PRT: 223 AA.

AC QYUJF605; PRELIMINARY; PRT: 223 AA.

DT 01-NOV-1998 (TREMBlrel. 08, created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE EXCNUCLEASE ABC SUBUNIT A (FRAGMENT).

GN UVRA.

OS Prevotella albensis.

OC Bacterii; CFB group; Bacteroidaceae; Prevotella.

OX NCBI_TaxID:77768;

RN [1]

RP SOURCE OF 9-191 FROM N.A.

RC STRAIN=M84;

RA Walker N.D., McEwan N.R., Wallace R.J.;

RT "Prevotella albensis putative uvrA gene." Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF070930; AAC24131.2; -.

DR INTERPRO; IPR001617; -.

DR PROSITE; PS00211; ABC_TRANSPORTER; 1.

RT ATP-binding; Transport; 1.

FT NON_TER 223 223

FT SEQUENCE 223 AA; 24579 MW; 2563BA0B0C2996C9 CRC64;

Query Match 30.5%; Score 53; DB 2; Length 223;
 Best Local Similarity 39.5%; Pred. No. 5.5; Matches 15; Conservative 1; Mismatches 4; Indels 1B; Gaps 2;

QY 11 RTDIDNPAPWYG-----RGGRPVGREF 31

ID 11 RTDIDNPAPWYG-----RGGRPVGREF 31

AC 11 RTDIDNPAPWYG-----RGGRPVGREF 31

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE SUSHI-REPEAT PROTEIN.

GN SRPUL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SOURCE FROM N.A.

RA Kurozawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T., Rakeström K.-M., Navee C.W., Look T.A.;

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF060567; AAC15765.1; -.

INTERPRO; IPR000436; -.

INTERPRO; IPR001128; -.

PFAM; PF00084; sushi; 3.

DR PROSITE; PS00866; CYTOCHROME_P450; UNKNOWN_1.

FT SEQUENCE 465 AA; 52971 MW; 4D752B187FF3EFB CRC64;

Query Match 30.5%; Score 53; DB 4; Length 465;
 Best Local Similarity 50.0%; Pred. No. 1.2;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 12 TPDINPAWVGRGIRP 27

Db 18 TPAVIPTWAGSGVYP 33

RESULT 9

QYLSC6 PRELIMINARY; PRT: 503 AA.

ID QYLSC6 PRELIMINARY; PRT: 503 AA.

AC QYLSC6; PRELIMINARY; PRT: 503 AA.

DT 01-OCT-2000 (TREMBlrel. 15, created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE EMB|CGB75482.1

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SOURCE FROM N.A.

RC STRAIN=COLOMBIA;

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RT [2]

RP SOURCE FROM N.A.

RC STRAIN=M84;

RA Nakamura Y.;

RT "structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty PI and TAC clones.";

RL DNA Res. 7.131-135(2000).

DR EMBL; AB026649; BAB01091.1; -.

SO SEQUENCE 503 AA; 57928 MW; F5E38CD1BA9C521A CRC64;

Query Match 29.9%; Score 52; DB 10; Length 503;
 Best Local Similarity 33.3%; Pred. No. 18; Matches 9; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY	3	AHQHSMETRTPDINPAWYTGRGIRPVG	29
Db	199	AHQHNLMSFSKDSEESNECCGACVPRIG	225
RESULT	10		
Q9KUW5		PRELIMINARY;	PRT; 940 AA.
ID	Q9KUW5		
AC	Q9KUW5;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	EXCINUCLEASE ABC, SUBUNIT A.		
GN	VC0394.		
OS	Vibrio cholerae.		
OC	Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.		
OX	NCBI_TAXID=666;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=EL TOR NI6961 / SEROTYPE O1;		
RX	MEDLINE=20406813; PUBMED=10952301;		
RA	Heidelberg J.P., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.R., Peterson J.D., Umayam L.A., McDonald L.L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Gill S.R., Nelson C.E., Read T.D., Tettelin H., Richardson D., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;		
RA	"DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae."		
RL	Nature 406:477-483(2000).		
DR	AE04127; ARF93567; 1; -.		
DR	TIGR: VC0394; 1A; 104327 MW; 84F93B9DF686F6F2 CRC64;		
SO	SEQUENCE: 940 AA; 29.9%; Score 52; DB 2; Length 940; Best Local Similarity 39.5%; Pred. No. 36; Matches 15; Conservative 1; Mismatches 4; Indels 18; Gaps 2;		
Db	694 RTPRSNPATYTGIFTPIREFLAGTQESRSRGYDP-GRF 730		
RESULT	11		
Q9KRV1		PRELIMINARY;	PRT; 503 AA. -
ID	Q9KRV1		
AC	Q9KRV1;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	SUNNUCLEOLAR PROTEIN FAMILY PROTEIN.		
GN	VC1502.		
OS	Vibrio cholerae.		
OC	Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.		
OX	NCBI_TAXID=666;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=EL TOR NI6961 / SEROTYPE O1;		
RX	MEDLINE=20406813; PUBMED=10952301;		
RA	Heidelberg J.P., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.R., Peterson J.D., Umayam L.A., Gill S.R., Nelson C.E., Read T.D., Tettelin H., Richardson D., McDonald L.L., Utterback T., Bass S., Qin H., Dragoi I., Sailers P., McDaniel L., Utterback T., Fleishmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;		
RA	"DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae."		
RT	Nature 406:477-483(2000).		
RT	"EMBL: AB004228; ARF94657; 1; -.		
RESULT	12		
Q9KU50		PRELIMINARY;	PRT; 294 AA.
ID	Q9KU50		
AC	Q9KU50;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-OCT-2000 (TREMBLrel. 10, Last sequence update)		
DE	F1986.1. PROTEIN.		
GN			
OS	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Caenorhabditis elegans.		
OC	Rhabditidae; Peleoriniae; Caenorhabditis.		
RA	Rhabditida; Peleoriniae; Caenorhabditis.		
RP	SEQUENCE FROM N.A.		
RL	Submitted (Aug-1995) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL: Z50873; CAM90762.1; JOINED.		
DR	EMBL: Z68115; CAM90762.1; JOINED.		
DR	EMBL: Z68115; CAM92165.1; JOINED.		
DR	EMBL: Z50873; CAM92169.1; JOINED.		
DR	HSSP: F24941; ICAP.		
DR	INTERPRO: IPR000719; -.		
DR	INTERPRO: IPR001245; -.		
DR	INTERPRO: IPR002290; -.		
DR	PRINTS: PF0009; kinase_1.		
DR	PRINTS: PRO0109; TYRKINASE.		
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.		
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.		
DR	PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.		
SQ	SEQUENCE: 294 AA; 34006 MW; 071DA6644D049F43 CRC64;		
RESULT	13		
Q9DUQ49		PRELIMINARY;	PRT; 428 AA.
ID	Q9DUQ49		
AC	Q9DUQ49;		
DT	01-MAR-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		
DE	GANGLIOSIDE STARCHIDASE.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OX	NCBI_TAXID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-BRAIN.		
RA	Wada T., Yoshikawa Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T.;		
RT	"Cloning, expression, and chromosomal mapping of a human ganglioside sialidase."		

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RL Bioclim. Biophys. Res. Commun. 261:21-27 (1999).
 DR EMBL: AB008185; BAA82611.1; -.
 DR EMBL: AB008185; BAA82611.1; -.
 DR INTERPRO: IPR00260; -.
 DR INTERPRO: IPR00345; -.
 DR PFAM: PF02012; BNR: 3.
 SEQUENCE 428 AA; MW: 35DIDDD9359A7BC98 CRC64:
 50 SROINCR: 176 AA; 19727 MW; 4D99C97A690BA0 CRC64;
 DR EMBL: Z75161; CAA99475.1; -.
 DR INTERPRO: IPR00182; -.
 DR INTERPRO: IPR00345; -.
 DR PFAM: PF00583; Acetyltransf_1.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR SROINCR: 176 AA; 19727 MW; 4D99C97A690BA0 CRC64;

	Query Match	29.3%	Score 51; DB 4; Length 428;
	Best Local Similarity	33.3%	Pred. No. 21; Mismatches 9; Conservative
Matches	9;	Indels 12; Gaps 0;	Mismatches 6;
Qy	2 RAHQHSMETRDPIDINPAWYTGRGIRPV 28		
:	: : : :		
Db	195 KTRPHSLMYSDDLGVTWHGRLLRPW 221		
	Query Match	29.0%	Score 50.5; DB 3; Length 176;
	Best Local Similarity	31.2%	Pred. No. 9.8; Mismatches 10; Conservative
Matches	10;	Indels 4; Gaps 15;	Mismatches 15;
Qy	1 SRAHQHSMETRDP--DINPAWYTGRGIRPVG 29		
:	: : : :		
Db	120 SECHQHNPVYLPAPVDDLTQKWFIAHGFECVG 151		

ONGEL PRELIMINARY; PRT; 529 AA.
 ID ONGEL; AC
 AC ONGEL;
 DT 01-OCT-2000 (EMBL:REI. 15, Created)
 DT 01-OCT-2000 (EMBL:REI. 15, Last sequence update)
 DT 01-OCT-2000 (EMBL:REI. 15, Last annotation update)
 DE NURAMINTASE (EC 3.2.1.10).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9605;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Monti E., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerando B.,
 RA Croci G., Preti A., Baimbio A., Tettamanti G., Borsani G.;
 RT "Identification and expression of NEUD3, a novel human sialidase
 associated to the plasma membrane.";
 RL Biochem. J. 349:343-351(2000).
 DR EMBL: Y1B633; CAB96131.1; -.
 KW Hydrolase; Glycosidase.
 SEQUENCE 629 AA; 59702 MW; 97C5464B70E69B4B CRC64;
 SQ

Query Match	29.3%	Score	51	DB	4	Length	629
Best Local Similarity	33.3%	Pred. No.	32				
Matches	9	Conservative	6	Mismatches	12	Indels	0
Oy	2 RAHQHSMETRPIDNPANYTGRGTRPV 28					Gaps	0
Db	396 KTRPHLSMLYSDDDGVTWHRGRJRP 422						

W0003	Q08689	PRELIMINARY;	PRT;	176 AA.
AC	Q08689;			
DT	01-NOV-1996 (TREMBLrel).	01. Created)		
DT	01-NOV-1996 (TREMBLrel).	01. Last sequence up-		
DT	01-OCT-2000 (TREMBLrel).	15. Last annotation		
DE	CHROMOSOME XV READING FRAME ORF P953W.			
OS	Saccharomyces cerevisiae (Baker's Yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycete			
OC	Saccharomycetidae; Saccharomyces.			
OX				
RN	NCBI_TAXID=4932;			
RR	[1]			
RP	SEQUENCE FROM N.A.			
RA	MIPS;			
RL	Submitted (JUL-1996) to the EMBL/GenBank/DDBJ			

RA Jauniaux J.C., Poirey R.;
 RT "Sequencing analysis of a 36.8 kb fragment of yeast chromosome XV
 reveals 26 open reading frames including SEC63, COC31, SUG2, GCD1,
 RYB2, PNT1, PAC1 and VHL";
 RL Yeast. 13:483-487(1997).

Tue Apr 17 15:46:12 2001

us-09-446-543a-47.rspt

Gencore version 4.5									
Copyright (c) 1993 - 2000 Compugen Ltd.									
W protein - protein search, using sw model									
Search time 39.1 Seconds (without alignments) 27.159 Million cell updates/sec									
April 17, 2001, 15:48:47 : Search time 39.1 Seconds (without alignments) 27.159 Million cell updates/sec									
erfect score:	US-09-446-543A-47	174	1	SRAHOHSMETRDPIDINPAWYGRGIRPVGRF	31				
oring table:	BLOSUM62								
searched:	Gapox 10.0 , Gapext 0.5								
post-processing:	Minimum Match 0 %								
atabase :	Maximum Match 100%								
	Listing first 45 summaries								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
result NO.	Score	% Match	Length	DB	ID	Description			
1	174	100.0	83	1	PRRP-RAT	P81278 rattus norvegicus	PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE	1	STANDARD; PRT; 83 AA.
2	163	93.7	98	1	PRL-BOVIN	P81264 bos taurus	PEPTIDE PRRP2; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
3	149	85.6	87	1	PRRP-HUMAN	P81277 homo sapien	PEPTIDE PRRP3; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
4	56	32.2	962	1	UVRA-METH	O26543 methanobacter	PEPTIDE PRRP4; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
5	53	30.5	798	1	UNR-RAT	P18895 rattus norvegicus	PEPTIDE PRRP5; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
6	52	29.9	972	1	UVRA-MYCNU	P94972 mycobacterium	PEPTIDE PRRP6; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
7	52	29.9	973	1	UVRA-RHIME	P56899 rhizobium	PEPTIDE PRRP7; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
8	51	29.3	943	1	UVRA-HAEM	P44410 haemophilus	PEPTIDE PRRP8; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
9	50	28.7	264	1	Y355-BUCNAI	P57436 buchnera apicola	PEPTIDE PRRP9; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
10	50	28.7	482	1	R167-YEAST	P39743 saccharomyces cerevisiae	PEPTIDE PRRP10; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
11	50	28.7	940	1	UVRA-ECOLI	P07671 escherichia coli	PEPTIDE PRRP11; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
12	50	28.7	941	1	UVRA-SALTY	P37434 salmonella enterica	PEPTIDE PRRP12; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
13	50	28.7	953	1	UVRA-RICOR	O22cc3 rickettsia	PEPTIDE PRRP13; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
14	49.5	28.4	374	1	YHR-ECOJI	P31993 escherichia coli	PEPTIDE PRRP14; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
15	49	28.2	952	1	UVRA-THERT	O26242 thermus aquaticus	PEPTIDE PRRP15; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
16	49	28.2	970	1	UVRA-SYNX3	P73412 synchocystis	PEPTIDE PRRP16; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
17	49	28.2	1014	1	UVRA-STROCI	O22507 streptomyces	PEPTIDE PRRP17; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
18	48	27.6	569	1	UVRA-VISTT	P06518 vitreoscilla	PEPTIDE PRRP18; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
19	48	27.6	719	1	ARP YEAST	P27770 saccharomyces	PEPTIDE PRRP19; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
20	48	27.6	798	1	UNR-HUMAN	P07534 homo sapiens	PEPTIDE PRRP20; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
21	48	27.6	950	1	UVRA-NEIGO	P051968 neisseria gonorrhoeae	PEPTIDE PRRP21; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
22	48	27.6	960	1	UVRA-TREPAA	O28347 treponema pallidum	PEPTIDE PRRP22; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
23	48	27.6	1194	1	BCHE-RHOEA	P26162 rhodobacter	PEPTIDE PRRP23; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
24	47.5	27.3	501	1	TRAZ-MOUSE	P34429 mus musculus	PEPTIDE PRRP24; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
25	47.5	27.3	941	1	GCSP-MYCUT	P05601 mycobacterium	PEPTIDE PRRP25; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
26	47	27.0	453	1	TBB2-GEOCN	P12925 geotrichum	PEPTIDE PRRP26; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
27	47	27.0	926	1	UVRA-AQUAE	O69911 aquilegia	PEPTIDE PRRP27; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
28	47	27.0	1083	1	T2D3-HUMAN	P002668 homo sapiens	PEPTIDE PRRP28; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
29	46.5	26.7	272	1	TRA2-DROVI	P002008 drosophila melanogaster	PEPTIDE PRRP29; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
30	46.5	26.7	652	1	TETP-CIOPPE	P043306 clostridium perfringens	PEPTIDE PRRP30; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
31	46	26.4	322	1	GRP2-MOUSE	O89100 marmoset	PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
32	46	26.4	330	1	GRP2-HUMAN	O75791 h. griseus	PEPTIDE PRRP32; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
33	46	26.4	925	1	UVRA-ZYMO	O31151 zymomonas	PEPTIDE PRRP33; PROLACTIN-RELEASING PEPTIDE PRRP1; PROLACTIN-RELEASE		
RESULT	2								
ALIGNMENTS									
44.5	25.6	240	1	PLSC_HELPY	O252903 helicobacter	O252903 helicobacter	O252903 helicobacter		
45	44.5	25.6	1	DPOL_THEFM	P74918 thermococcus	P74918 thermococcus	P74918 thermococcus		
45	44	25.9	1523	1	DPOL_THEGO	P36689 thermococcus	P36689 thermococcus	P36689 thermococcus	
45	45	25.9	676	1	EXII_HUMAN	P7370 saccharomyces	P7370 saccharomyces	P7370 saccharomyces	
45	45	25.9	773	1	YRL1_YEAST	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	817	1	YAE9_SCHPO	P034863 bacillus subtilis	P034863 bacillus subtilis	P034863 bacillus subtilis	
45	45	25.9	430	1	YRL6_THEMLA	P075758 escherichia coli	P075758 escherichia coli	P075758 escherichia coli	
45	45	25.9	184	1	YRL7_THEMLA	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	126	1	YRL8_ECOLI	P075758 escherichia coli	P075758 escherichia coli	P075758 escherichia coli	
45	45	25.9	1016	1	YRL9_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL10_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL11_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL12_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL13_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL14_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL15_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL16_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
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45	45	25.9	1016	1	YRL20_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL21_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL22_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
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45	45	25.9	1016	1	YRL32_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
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45	45	25.9	1016	1	YRL38_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL39_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
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45	45	25.9	1016	1	YRL45_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL46_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL47_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL48_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL49_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL50_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
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45	45	25.9	1016	1	YRL56_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL57_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL58_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL59_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL60_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL61_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL62_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL63_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL64_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL65_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL66_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL67_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL68_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL69_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL70_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45	25.9	1016	1	YRL71_HUMAN	P09849 schizophyllum	P09849 schizophyllum	P09849 schizophyllum	
45	45</td								

PRP_BOVIN	ID PRP_BOVIN	STANDARD;	PRT; 98 AA.
	FB12264;		
	AC 30-MAY-2000 (Rel. 39, Created)		
	DT 30-MAY-2000 (Rel. 39, Last sequence update)		
	DT 30-MAY-2000 (Rel. 39, Last annotation update)		
	DE PROLACTIN-RELEASING PEPTIDE PRECURSOR (PRRP) (PROLACTIN-RELEASING HORMONE) (CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20).		
	DE PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20).		
	GN PRH.		
	OS Bos taurus (Bovine).		
	OC Bos taurata; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
	OC NCBI_TaxID=9913;		
	RN [1]		
	RP TISSUE=Brain;		
	RC SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.		
	RX MEDLINE=98268781; PubMed=907765;		
	RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Oda H., Fujino M.;		
	RA "A prolactin-releasing peptide in the brain."		
	RT Nature 393:272-276(1998).		
	CC EXPRESSION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.		
	CC -1- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.		
	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
	CC DR EMBL: AB0115419; BAA29027.1; -.		
	CC DR MIM: 603663; -.		
	CC KW Hormone; Amidation; Signal.		
	CC FT SIGNAL; 1 22.		
	CC FT PEPTIDE; 23 53.		
	CC FT PEPTIDE; 34 53.		
	CC FT MOD_RES 53 53.		
	CC SQ SEQUENCE 87 AA; 9639 MW; 22942F3F50CF981B CRC64;		
	CC EMBL: AB0115417; BAA2025.1; -.		
	CC DR MIM: 603663; -.		
	CC KW Hormone; Amidation; Signal.		
	CC FT SIGNAL; 1 22.		
	CC FT PEPTIDE; 23 53.		
	CC FT PEPTIDE; 34 53.		
	CC FT MOD_RES 53 53.		
	CC SQ SEQUENCE 87 AA; 9639 MW; 22942F3F50CF981B CRC64;		
	CC EMBL: AB0115417; BAA2025.1; -.		
	CC DR MIM: 603663; -.		
	CC KW Hormone; Amidation; Signal.		
	CC FT SIGNAL; 1 22.		
	CC FT PEPTIDE; 23 53.		
	CC FT PEPTIDE; 34 53.		
	CC FT MOD_RES 53 53.		
	CC SQ SEQUENCE 87 AA; 9639 MW; 22942F3F50CF981B CRC64;		
	Query Match RESULT 4		
	URMETH ID URMETH	STANDARD;	PRT; 962 AA.
	AC 026543;		
	DT 30-MAY-2000 (Rel. 39, Created)		
	DT 30-MAY-2000 (Rel. 39, Last sequence update)		
	DT 30-MAY-2000 (Rel. 39, Last annotation update)		
	GN UYRA OR MTH43.		
	OC Methanobacterium thermoautotrophicum.		
	OC Archaeal; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;		
	OC NCBI_TaxID=145262;		
	RN [1]		
	RP SEQUENCE FROM N.A.		
	RC SRRAIN-DELTA_H;		
	RX MEDLINE=98037514; PubMed=9371453;		
	RA Smith D.R., Doucette-Stamm L.A., Detoughere C., Lee H.-M., DuBois J., Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lamm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Probhakar S., McDouall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-T., Rice P., Nolling J., Reeve J.N., De Prolacitin-releasing Peptide Precursor (PRRP) (PROLACTIN-RELEASING HORMONE) (CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20).		
	DE PROLACTIN-RELEASING PEPTIDE PRECURSOR (PRRP) (PROLACTIN-RELEASING HORMONE) (CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20).		
	DE PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20).		
	GN PRH.		
	OS Homo sapiens (Human).		
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	OC NCBI_TaxID=9606;		
	RN [1]		
	RP SEQUENCE FROM N.A.		
	CC TISSUE=Brain;		
	CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UYRA IS AN ATPASE AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).		
	CC -1- SUBUNIT: CONSISTS OF THREE SUBUNITS: UYRA, UYRB AND UYRC.		
	CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).		
	CC CATALYZES THE EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT		
	CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UYRA IS AN ATPASE AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).		
	CC -1- SUBUNIT: CONSISTS OF THREE SUBUNITS: UYRA, UYRB AND UYRC.		
	CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING PROTEIN FAMILY		

CC (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

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CC EMBL; AE000828; AA884949_1; -.

DR InterPro; IPR001617; -.

DR Pfam; PF0005; ABC_tran; 2.

DR PROSITE; PS00211; ABC_TRANSPORTER; 2. repair; ATP-binding; Repeat;

KW SOS response; Excision nuclelease; DNA repair; ATP-binding; Repeat;

KW DNA-binding; Zinc-finger.

FT NP_BIND 38 45 ATP (POTENTIAL).

FT NP_BIND 549 655 ATP (POTENTIAL).

FT ZN_FING 748 774 CA-ATPE.

SO SEQUENCE 962 AA; 108395 MW; 200EF7FC41CCD060 CRC64;

Query Match 32.2%; Score 56; DB 1; Length 962; Best Local Similarity 42.1%; Pred. No. 2.5; Matches 16; Conservative 0; Mismatches 4; Indels 18; Gaps 2;

OY 11 RTPDPINPAWTG-----RGIREVGRF 31

Db 703 RTPRSNPATVGYVHIRELFAQTPEARKGKGRP-GRF 739

RESULT 5

UNR_RAT STANDARD; PRT; 798 AA.

ID UNR_RAT

AC P18395; 01-NOV-1990 (Ref. 16, Created) 01-OCT-2000 (Ref. 40, Last annotation update)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE EXTRNUCLEASE ABC SUBUNIT A

GN UVRA OR RV1138 Or MTC06H11.02.

OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae; Actinomycetales; Corynebacteriaceae; Mycobacterium.

OX NCBI_TAXID=1773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RA MEDLINE=9825987; Pubmed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas J., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Ralbandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. *Nature* 393:537-544 (1998).

CC TISSUE=TESTIS; MEDLINE=9307473; PubMed=2204629;

RA Jeffers M., Paciucci R., Pellicer A.; Characterization of unr, a gene closely linked to N-ras.; Nucleic Acids Res. 18:4891-4893(1990).

RL -1- FUNCTION: RNA-BINDING PROTEIN (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.

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CC EMBL; X52311; CA836549_1; -.

DR InterPro; IPR002059; -.

DR Pfam; PF00313; CSD; 8.

DR PROSITE; PS00352; COLD_SHOCK; 4.

KW RNA-binding; Repeat.

FT DOMAIN 25 87 CSD 1. (INCOMPLETE).

FT DOMAIN 136 179 CSD 2. (INCOMPLETE).

FT DOMAIN 186 245 CSD 3.

FT DOMAIN 297 337 CSD 4 (INCOMPLETE).

FT DOMAIN 349 410 CSD 5.

FT DOMAIN 447 507 CSD 6.

FT DOMAIN 519 579 CSD 7.

FT DOMAIN 610 670 CSD 8.

FT DOMAIN 674 735 CSD 9.

FT DOMAIN 798 AA; 88894 MW; F484B3TA8B0995A4 CRC64;

Query Match 30.5%; Score 53; DB 1; Length 798; Best Local Similarity 43.5%; Pred. No. 5.5; Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 6 HSEMETRPDPINPAWTGGRGIRPV 28

Db 583 HSYGNTEEANTPIVSKVREL 605

RESULT 6

UVRA_MYCTU STANDARD; PRT; 972 AA.

ID UVRA_MYCTU

AC P94972; 15-DEC-1998 (Rel. 37, Created) 30-MAY-2000 (Rel. 39, Last annotation update)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE EXTRNUCLEASE ABC SUBUNIT A

GN UVRA OR RV1138 Or MTC06H11.02.

OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae; Actinomycetales; Corynebacteriaceae; Mycobacterium.

OX NCBI_TAXID=1773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RA MEDLINE=9825987; Pubmed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas J., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Ralbandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. *Nature* 393:537-544 (1998).

CC TISSUE=TESTIS; MEDLINE=9307473; PubMed=2204629;

RA Jeffers M., Paciucci R., Pellicer A.; Characterization of unr, a gene closely linked to N-ras.; Nucleic Acids Res. 18:4891-4893(1990).

RL -1- FUNCTION: RNA-BINDING PROTEIN (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.

CC CATALyzes the excision reaction of UV-damaged nucleotide segments producing oligomers having the modified base(s). UVRA is an ATPase and a DNA-binding protein that preferentially binds single-stranded or UV-irradiated double-stranded DNA (BY SIMILARITY).

CC -1- SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRC.

CC -1- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALyzes the excision reaction of UV-damaged nucleotide segments producing oligomers having the modified base(s). UVRA is an ATPase and a DNA-binding protein that preferentially binds single-stranded or UV-irradiated double-stranded DNA (BY SIMILARITY).

CC -1- SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRC.

CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

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CC EMBL; Z8982; CAB00633_1; -.

DR Tuberculist; Ry1538; -.

DR InterPro; IPR001617; -.

DR Pfam; PF00005; ABC_tran; 2.

DR PROSITE; PS00211; ABC_TRANSPORTER; 2. repair; ATP-binding; Repeat;

KW SOS response; Excision nuclelease; DNA repair; ATP-binding; Repeat;

KW DNA-binding; Zinc-finger.

FT NP_BIND 32 39 ATP (POTENTIAL).

FT NP_BIND 654 661 ATP (POTENTIAL).

Query Match 29.9%; Score 52; DB 1; Length 973;
 Best Local Similarity 39.5%; Pred. No. 9.4;
 Matches 15; Conservative 1; Mismatches 4; Indels 18; Gaps 2;

OY 11 RTPDINPAWYG-----RGIRPGRF 31
 Db 708 RTPRSRHPATVGFVDKIRTFAAITEAKVGRGQP-GRF 744

RESULT 7 .
 UVRA_RHIME STANDARD; PRT: 973 AA.
 AC P56895;
 DT 30-MAY-2000 (Rel. 3.9, Created)
 DT 30-MAY-2000 (Rel. 3.9, Last sequence update)
 DT 30-MAY-2000 (Rel. 3.9, Last annotation update)
 DE EXCINUCLEASE ABC SUBUNIT A.
 GN UVRA.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria: Proteobacteria: alpha subdivision: Rhizobiaceae group;
 OC Rhizobiales: Rhizobiaceae: Sinorhizobium.
 OX NCBI_TAXID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RA Galibert F., Capela D., Huber-Biloy F., Gatius M., Batut J.,
 RA Boistard P., Couzy J., Kahn D., Thebaud P., Goffeau A.,
 RA Purnelle B., Pohl T., Botte G., Schneider S., Portetelle D.,
 RA Vandembrou M., Puehler A., Becker A., Weidner S.;
 RL Submitted (MAY-2000) to the SWISS-PROT data bank.
 RN [2]
 RP SEQUENCE OF 1-140 FROM N.A.
 RC STRAIN=2021;
 RX MEDLINE=99430868; PubMed=10503543;
 RA Tapas A., Barbe J.;
 RT "Regulation of divergent transcription from the uvra-ssb promoters in
 Sinorhizobium meliloti";
 Mol. Gen. Genet. 262:121-130(1999),
 CC CATALYZES THE EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
 CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN APNASE
 CC AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-
 CC STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
 -1- SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRD.
 -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

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 or send an email to license@isb-sib.ch).

CC DR EMU; AF125162; AAF03210.1; - .
 DR InterPro; IPRE001617; TRANSPORTER; PARTIAL.
 DR PROSITE; PS00211; ABC-TRANSPORTER; PARTIAL.
 KW SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat;
 KW DNA-binding; Zinc-finger.

FT NP_BIND 34 41 ATP (POTENTIAL).
 FT NP_BIND 662 669 ATP (POTENTIAL).
 FT ZN_FING 761 787 C4-TYPE.
 FT CONFLICT 19 19 G -> A (IN REF. 2).
 FT CONFLICT 67 67 F -> S (IN REF. 2).
 SEQUENCE 973 AA; 107191 MW; 3E1A8B14527A7FE CRC64;

Query Match 29.9%; Score 52; DB 1; Length 973;
 Best Local Similarity 39.5%; Pred. No. 9.4;
 Matches 15; Conservative 1; Mismatches 4; Indels 18; Gaps 2;

OY 11 RTPDINPAWYG-----RGIRPGRF 31
 Db 716 RTPRSNPATVTFGFTPLRDWFAGLPEAKVGRGQP-GRF 752

RESULT 8 .
 UVRA_HAEIN STANDARD; PRT: 943 AA.
 AC P44410; Q48151;
 DT 01-NOV-1995 (Rel. 3.2, Created)
 DT 01-NOV-1995 (Rel. 3.2, Last sequence update)
 DT 30-MAY-2000 (Rel. 3.9, Last annotation update)
 DE EXCINUCLEASE ABC SUBUNIT A.
 GN UVRA OR HI0249.
 OS Haemophilus influenzae.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TAXID=727;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=9530630; PUBMED=542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Krikness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., FitzHugh W., Fields C.R., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Springs T., Heidelberg E., Cottrell M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fungmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.,
 RT "whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd. ";
 RL Science 269:495-512(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NTHI TN106;
 RX MEDLINE=94341556; PubMed=8063092;
 RA Jarosik G.P., Hansen E.J.,
 RT "Cloning and sequencing of the Haemophilus influenzae ssb gene
 encoding single-stranded DNA-binding protein";
 RL Gene 146:101-103(1994).
 CC CATALYZES THE EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
 CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN APNASE
 CC AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-
 CC STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
 -1- SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRD.
 -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

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 or send an email to license@isb-sib.ch).

Query Match 28.7%; Score 50; DB 1; Length 264;
 Best Local Similarity 41.7%; Pred. No. 4.7; Indels 0; Gaps 0;
 Matches 10; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 8 MMTTPDPINPAWYTGGRGIRPVGRF 31
 DB 210 IETDSPILSPAPYRGRKGKGNOPAYLF 233

Query Match 29.3%; Score 51; DB 1; Length 943;
 Best Local Similarity 39.5%; Pred. No. 13; Indels 18; Gaps 2;
 Matches 15; Conservative 0; Mismatches 5; Indels 18; Gaps 2;

Qy 11 RPPDPINPAWYTGGRGIRPVGRF 31
 DB 695 RPPRSNPATVTLGLFPIRELFLAGVEARARGYNP-GRF 731

RESULT 9
 ID Y355_BUCAT STANDARD; PRT: 264 AA.
 AC F57436; (rel. 40, Created)
 DT 01-OCT-2000 (rel. 40, Last sequence update)
 DT 01-OCT-2000 (rel. 40, Last annotation update)
 DE PUTATIVE DEOXYRIBONUCLEASE BU355 (EC 3.1.21.-).
 GN GN355.
 OS Buchnera aphidicola (subsp. *Acyrthosiphon pisum*) (*Acyrthosiphon pisum* symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TAXID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TOKYO 1998;
 RX MEDLINE=20451173; PubMed=1093077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS";
 RL Nature 407:81-86(2000).
 CC -1 SIMILARITY: BELONGS TO THE TADP DNASE FAMILY. STRONG, TO E.COLI
 CC YCPH.

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EMBL: AP001119; BAB13059.1; -.
 PROSITE: PS01137; TADP_1; 1.
 PROSITE: PS01090; TADP_2; 1.
 PROSITE: PS01091; TADP_3; FALSE_NEG.
 Hypothetical protein; Hydrolase; Nuclease.
 SEQUENCE 264 AA; 30520 MW; 7f1Da900018E0AAC CRC64;

Query Match 29.3%; Score 51; DB 1; Length 943;
 Best Local Similarity 39.5%; Pred. No. 13; Indels 18; Gaps 2;
 Matches 15; Conservative 0; Mismatches 5; Indels 18; Gaps 2;

Qy 9 MMTTPDPINPAWYTGGRGIRPVGRF 31
 DB 943 AA; 104366 MW; 4DBA0DCFA602D465 CRC64;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TOKYO 1998;
 RX MEDLINE=93360299; PubMed=8336735;
 RA Bauer F., Urdaci M., Aigle M., Crouzet M.;
 RT "Alteration of a yeast SH3 protein leads to conditional viability with defects in cytoskeletal and budding patterns.;"
 RL Mol. Cell. Biol. 13:5070-0084 (1993).
 [2]
 RN SEQUENCE FROM N.A.
 RP DIERTRICH F.S., MULIGAN J., ALLEN E., ARAUJO R., AVILES E.,
 RA BERNO A., CARPENTER J., CHEN E., CHERRY J.M., CHUNG E., DUNCAN M.,
 RA HUNICKE-SMITH S., HYMAN R., KOMP C., LASHKARI D., LEW H., LIN D.,
 RA MOSEDALE D., NAKAMURA K., NAMATH A., OEFNER P., OH C., PEETEL F.X.,
 RA ROBERTS D., SCHRAMM S., SCHROEDER M., SHAGREN T., SHROFF N.,
 RA WILANT A., YELTON M., BOTSTEIN D., DAVIS R.W.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP ACTIN-BINDING.
 RX MEDLINE=95236199; PubMed=7719850;
 RA AMBERG D.C., BASSET E., BOTSTEIN D.;
 RT "Defining protein interactions with yeast actin in vivo.";
 RL Struct. Biol. 2:26-35(1995).
 CC -1 FUNCTION: COMPONENT OF A CYTOSKELETAL STRUCTURE THAT IS REQUIRED FOR THE FORMATION OF ENDOCYTIC VESICLES AT THE PLASMA MEMBRANE LEVEL. COULD BE IMPLICATED IN CYTOSKELETAL REORGANIZATION IN RESPONSE TO ENVIRONMENTAL STRESSES AND COULD ACT IN THE BUDGING SITE SELECTION MECHANISM. BLINDS TO ACTIN.
 CC -1 SIMILARITY: TO YEAST RVS161.
 CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC EMBL: M92092; AAA35051.1; -.
 DR EMBL: U32274; ARB64830.1; -.
 DR PIR: S40887; S40887.
 DR HSSP: P04002; LATF.
 DR SGD: S0002796; RVS167.
 DR InterPro: IPRO01452; -.
 DR Pfam: PF0018; SH3; 1.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS50002; SH3; 1.
 KW Cytoskeleton; SH3 domain; Transmembrane; Actin-binding.
 FT DOMAIN 292 427 ALA/GLY/PRO-RICH.
 TRANSMEM 344 367 POTENTIAL.

FT DOMAIN 421; 482 AA; 52774 MW; SH3.

SO SEQUENCE 482 AA; 52774 MW; 3F0ab53EBCC95A5B CRC64;

Query Natch 28.7%; Score 50; DB 1; Length 482;
Best Local Similarity 50.0%; Pred. No. 8.8; Mismatches 2;
Matches 11; Conservative 3; Indels 6; Gaps 2;

Ov 11 RTPDINPAWYGR-----GIRP 27
Db 453 RPDVNV-EWNTGGRNGQGVFP 473

RESULT 11

ID UVRA_ECOLI STANDARD; PRT; 940 AA.

AC P07671; P76780; DT 01-APR-1988 (Rel. 07, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE EXCINUCLEASE ABC SUBUNIT A.

GN UVRA OR DINE.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86668204; PubMed=3007478;

RA Husain I., van Houten B., Thomas D.C., Sancar A.;
"Sequences of Escherichia coli uvra gene and protein reveal two potential ATP binding sites;"

RT J. Biol. Chem. 261:4895-4901(1986).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / NEI1655;
RX MEDLINE=94089392; PubMed=8265357;

RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.;
"Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes;"

RL Nucleic Acids Res. 21:508-517(1993).
[3]

RN [4]

RP SEQUENCE OF I-25 FROM N.A.

RX MEDLINE=83299251; PubMed=6310514;

RA Backendorf C., Brandsma J.A., Kartasova T., van de Putte P.;
"In vivo regulation of the uvra gene: role of the '-10' and '-35' promoter regions."

RT Nucleic Acids Res. 11:5795-5810(1983).

RL Nature 288:96-98(1982).
[5]

RN [6]

RP CHARACTERIZATION.

RX MEDLINE=1208117; PubMed=1826851;

RA Myles G.M., Sancar A.;
"Isolation and characterization of functional domains of Uvra;"
RL Biochemistry 30:3839-3840(1991).

RN [6]

RP MUTAGENESIS OF CYS-253.

RX MEDLINE=89380431; PubMed=2550431;

RA Narayanan S., Myles G.N., Strange R.W., Sancar A.;
"Evidence from extended X-ray absorption fine structure and site-specific mutagenesis for zinc fingers in Uvra protein of Escherichia coli;"
J. Biol. Chem. 264:16067-16071(1989).

CC :-! FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS PRODUCING OLIGOMERS NAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

CC AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA.

CC SUBUNIT: CONSISTS OF THREE SUBUNITS: UVRA, UVRB AND UVRC.

CC MISCELLANEOUS: Binds about 2 zinc atoms/molecule.

CC SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

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CC DR EMBL; UD0005; AAC3152; I; DR EMBL; UD0004; 9; AAC77028; 1; DR EMBL; X01621; CAM25764; 1; DR ENBL; J01721; RAM2753; 1; DR PIR; A23869; BVECRA.

CC DR ECO2DBASE; H124; 0; 6TH EDITION.

DR Ecogene; EG11061; UVRA.

DR InterPro; IPR001617; -.

DR Pfam; PF0005; ABC_tran; 2.

DR PROSITE; PS0211 ABC_TRANSPORTER; 2.

KW SOS RESPONSE; EXCISION NUCLEASE; DNA REPAIR; ATP-BINDING; Repeat; DNA-BINDING; ZINC-FINGER.

FT NP-BIND 31 38 ATP.

FT NP-BIND 640 647 ATP.

FT ZN_FING 253 280 CA-TYPE.

FT ZN_FING 740 766 C4-TYPE.

FT MUTAGEN 253 253 C>A,H,S: REDUCED ACTIVITY.

SO SEQUENCE 940 AA; 103867 MW; D61AAEB6514B960C CRC64;

RESULT 12

ID UVRA_SALTY STANDARD; PRT; 941 AA.

AC P37434; DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)

DE EXCINUCLEASE ABC SUBUNIT A.

UVRA.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OX NCBI_TaxID=602;

RN [1]

RP SEQUENCE FROM N.A.

RA Alberti M., Li Y.F., Sancar A., Hearst J.E.;
RL Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.

CC :-! FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).

CC SUBUNIT: CONSISTS OF THREE SUBUNITS: UVRA, UVRB AND UVRC.

CC SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

CC MISCELLANEOUS: Binds about 2 zinc atoms/molecule (BY SIMILARITY).

CC SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.

CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ235273; CAA15260_1; -.
 DR InterPro; IPR001617; -.
 DR Pfam; PF0005; ABC_tran; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 DR SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat;
 DR DNA-binding; Zinc-finger.
 KW ATP (POTENTIAL).
 FT NP_BIND 33 40 ATP (POTENTIAL).
 FT NP_BIND 652 659 ATP (POTENTIAL).
 FT 2N_BINDING 752 778 C4-TYPE.
 DR SEQUENCE 953 AA; 106287 MW; 6209A66241379421 CRC64;
 DR -----
 Query Match 28.7%; Score 50; DB 1; Length 941;
 Best Local Similarity 39.5%; Pred. No. 18;
 Matches 15; Conservative 0; Mismatches 5; Indels 18; Gaps 2;
 DR 11 RTPDINPAWYG-----RGRPVQRF 31
 QY 11 RTPDINPAWYG-----RGRPVQRF 31
 DR 695 RPRPSNPATVIGVFTPVRELEAGVPPSRSGXTP-GRF 731
 DR -----
 RESULT 13
 URA_RICPR STANDARD; PRT; 953 AA.
 ID URA_RICPR
 AC O9ZC33;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DR EXCINCHASE ABC SUBUNIT A.
 GN URA OR RP835.
 OS Rickettsia prowazekii.
 OC Rickettsiales; Rickettsiidae; Rickettsiaceae;
 OC Rickettsiae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MDR E:
 RX MEDLINE=9039499; PubMed=9823993;
 RA Andersson S.G.E., Zamorodipour A., Andersson J.O.,
 RA Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naelund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.",
 RL Nature 396:133-140(1998)
 CC -----
 -I- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
 CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
 PRODUCING OLIGONUCLEOTIDES HAVING THE MODIFIED BASE(S). URA IS AN ATPASE
 AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-
 STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
 CC -----
 -I- SUBUNIT: CONSISTS OF THREE SUBUNITS: URAA, URB AND URC.
 CC -----
 -I- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U00039; AAC18460_1; ALT_INIT.
 DR EMBL; AB00042; AAC78510_1; ALT_INIT.
 DR EMBL; I02370; AAC61886_1; -.
 DR Ecogene; EG11767; Yhhu.
 DR InterPro; IPR00012; -.
 DR PROSITE; PS00890; ABC2_MEMBRANE; 1.
 KW Hypothetical protein; Transport; Transmembrane; Inner membrane.
 FT TRANSMEM 23 43 POTENTIAL.

GenCore version 4.5
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run on: April 17, 2001, 15:39:47 ; Search time 61.54 Seconds
(without alignments)
9.677 Million cell updates/sec

title: US-09-146-543A-47
sequence: 1 SRAHRSMEITPDINPAWTFGRGIRPVGRR 31
scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 185757 seqs, 19210857 residues

total number of hits satisfying chosen parameters: 185757

minimum DB seq length: 0
maximum DB seq length: 200000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/laa/PCIUS_COMB.pep: *
6: /cgn2_6/ptodata/2/laa/backfilesl.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Length	DB ID	Description
1	174	100.0	31 3 US-09-105-678A-8	Sequence 8, Appli
2	174	100.0	31 3 US-09-105-678A-37	Sequence 37, Appli
3	174	100.0	31 4 US-09-172-353-4	Sequence 4, Appli
4	174	100.0	32 3 US-09-105-678A-38	Sequence 38, Appli
5	174	100.0	33 3 US-09-105-678A-39	Sequence 39, Appli
6	163	93.7	31 3 US-09-105-678A-31	Sequence 7, Appli
7	163	93.7	32 3 US-09-105-678A-32	Sequence 31, Appli
8	163	93.7	33 3 US-09-105-678A-33	Sequence 32, Appli
9	152	87.4	29 3 US-09-105-678A-29	Sequence 29, Appli
10	149	85.6	31 3 US-09-105-678A-9	Sequence 9, Appli
11	149	85.6	31 3 US-09-105-678A-43	Sequence 43, Appli
12	149	85.6	32 3 US-09-105-678A-44	Sequence 44, Appli
13	149	85.6	33 3 US-09-105-678A-45	Sequence 45, Appli
14	149	85.6	33 3 US-09-105-678A-46	Sequence 46, Appli
15	116	66.7	20 3 US-09-105-678A-40	Sequence 40, Appli
16	116	66.7	21 3 US-09-105-678A-41	Sequence 41, Appli
17	116	66.7	22 3 US-09-105-678A-42	Sequence 42, Appli
18	111	63.8	20 3 US-09-105-678A-34	Sequence 34, Appli
19	111	63.8	21 3 US-09-105-678A-35	Sequence 35, Appli
20	111	63.8	22 3 US-09-105-678A-36	Sequence 36, Appli
21	105	60.3	19 3 US-09-105-678A-30	Sequence 30, Appli
22	105	60.3	20 3 US-09-105-678A-46	Sequence 46, Appli
23	105	60.3	21 3 US-09-105-678A-47	Sequence 47, Appli
24	105	60.3	22 3 US-09-105-678A-48	Sequence 48, Appli
25	104	59.8	21 3 US-09-105-678A-28	Sequence 28, Appli
26	51	29.3	23 9 US-08-712-679A-7	Sequence 7, Appli
27	51	29.3	23 9 US-09-049-671-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-105-678A-8
Sequence 8, Application US/09105678A
Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suehaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P22
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Colin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-8

Query Match 100.0%; Score 174; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.5e-200
Matches 31; Conservative 0; Mismatches 0

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Db	1	SRAHOHSMETRUPDINPAWYTGRGIRPVGRP	31

; SEQ ID NO 4
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-172-353-4

US-09-105678A
; Sequence 37, Application US/09105678A
;
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Sunaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tamai, Yoko
APPLICANT: Nishimura, Osamu

	Matches	31;	Conservative	0;	Mismatches	0;	Indels	(
Oy	1	SRAHQHSMERTPDPINPANTGRGIRPVGRF	31					
Db	1	SRAHQHSMERTPDPINPANTGRGIRPVGRF	31					

CORRESPONDENCE ADDRESS:
ADDRESSEE: DJKE, BRONSTEIN, ROBERTS & CUSHMAN, LTD
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09/105,678A
FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-105,678A-37

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Query Match          100.0%; Score 174; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.5e-20; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
  1 SRAHQHSMETRDPDINPAWYTGRCIRPVGRF 31
  I SRAHQHSMETRDPDINPAWYTGRCIRPVGRF 31
Db

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RESULT 3

US-09-172353-4

; Sequence 4 Application US/09172353

; Patent No. 6197530

; GENERAL INFORMATION:

; APPLICANT: Stricker-Kongra, Alain

; APPLICANT: Gu, Wei

TITLE OF INVENTION: GPROT AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS

REGISTRATION NUMBER: 277,026
REFERENCE DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acid
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-38

Sequence 39, Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Patientin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 6
 US-09-105-678A-7
 Sequence 7, Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Patientin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-31

Query Match 93.7%; Score 163; DB 3; Length 31;
 Best Local Similarity 93.5%; Pred. No. 2.6e-18; 0; Mismatches 2; Indels 0; Gaps 0;
 Matches 29; Conservative ;
 QY 1 SRAHQHSMETRTPDINPAWYGRGIRPVGRF 31
 1 SRAHQHSMETRTPDINPAWYAGRGIRPVGRF 31
 Db 1 SRAHQHSMETRTPDINPAWYAGRGIRPVGRF 31

RESULT 8

US-09-105-678A-32

Sequence 32, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Sueyaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-105-678A-33

Query Match 93.7%; Score 163; DB 3; Length 33;

Best Local Similarity 93.5%; Pred. No. 2.8e-18; 0; Mismatches 2; Indels 0; Gaps 0;

Matches 29; Conservative ;

QY 1 SRAHQHSMETRTPDINPAWYGRGIRPVGRF 31
 1 SRAHQHSMETRTPDINPAWYAGRGIRPVGRF 31
 Db 1 SRAHQHSMETRTPDINPAWYAGRGIRPVGRF 31

RESULT 10

US-09-105-678A-29

Sequence 29, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Sueyaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

RESULT 9

Query Match 93.7%; Score 163; DB 3; Length 32;
 Best Local Similarity 93.5%; Pred. No. 2.7e-18; 0; Mismatches 2; Indels 0; Gaps 0;
 Matches 29; Conservative ;

QY 1 SRAHQHSMETRTPDINPAWYGRGIRPVGRF 31

Db 1 SRAHQHSMETRTPDINPAWYAGRGIRPVGRF 31

RESULT 9

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-9

INFORMATION FOR SEQ ID NO: 29:

Query Match 87.4%; Score 152; DB 3; Length 29;
 Best Local Similarity 93.1%; Pred. No. 1.1e-16;
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-29

Query Match 87.4%; Score 152; DB 3; Length 29;
 Best Local Similarity 93.1%; Pred. No. 1.1e-16;
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-29

RESULT 11
 US-09-105-678A-9

Sequence 9, Application US/09105678A
 Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu
 TITLE OR INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
 ADDRESSEE: DINE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-43

INFORMATION FOR SEQ ID NO: 43:

Query Match 85.6%; Score 149; DB 3; Length 31;
 Best Local Similarity 83.9%; Pred. No. 3.4e-16;
 Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-43

INFORMATION FOR SEQ ID NO: 43:

Query Match 85.6%; Score 149; DB 3; Length 31;
 Best Local Similarity 83.9%; Pred. No. 3.4e-16;
 Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-43

ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 9:

RESULT 13
 US-09-105-678A-44
 ; Sequence 44, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ; APPLICANT: Suemaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/105, 678A
 ; FILING DATE: 26-JUN-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 172118/1997
 ; FILING DATE: 27-JUN-1997
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/105, 678A
 ; FILING DATE: 26-JUN-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 172118/1997
 ; FILING DATE: 27-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conlin, David G.
 ; REGISTRATION NUMBER: 27,026
 ; REFERENCE/DOCKET NUMBER: 48466-342
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-105-678A-45
 ; INFORMATION FOR SEQ ID NO: 44:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 32 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: Peptide
 ; US-09-105-678A-44
 ;
 Query Match 85.6%; Score 149; DB 3; Length 32;
 Best Local Similarity 83.9%; Pred. No. 3.6e-16;
 Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 ;
 Qy I SRAHQHSMETRPPDINPAWYTRGIRPVGRF 31
 |||:||||| |||||:||| |||||:||| |||||:|||
 Db 1 SRTHRHSMEIRPDINPAWYASRGIRPVGRF 31
 ;
 ;
 RESULT 14
 US-09-105-678A-45
 ; Sequence 45, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ; APPLICANT: Suemaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/105, 678A
 ; FILING DATE: 26-JUN-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 172118/1997
 ; FILING DATE: 27-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conlin, David G.
 ; REGISTRATION NUMBER: 27,026
 ; REFERENCE/DOCKET NUMBER: 48466-342
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-40

Query Match 66.7%; Score 116; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TPDINPAWYGGRGIRPVGRF 31
||| | | | | | | | | | | | | |
Db 1 TPDINPAWYGGRGIRPVGRF 20

Search completed: April 17, 2001, 15:39:48
Job time: 317 sec



GenCore version 4.5
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OM Protein - protein search, using sw model

Run on: April 17, 2001, 15:38:42 ; search time 116.94 Seconds

{without alignments}
15.154 Million cell updates/secTitle: US-09-446-543A-47
Perfect score: 174
Sequence: 1 SRAHQISMETRPDINPAWYTGRGIRPVGRF 31Scoring table: BioSUM2
Gapext 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDSL/gcadata/geneseq/geneseq/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB ID	Description
1	174	100.0	Rat type G protein
2	174	100.0	Rat type ligand po
3	174	100.0	Rat 19p2 ligand
4	174	100.0	Murine pituitary-d
5	174	100.0	Murine pituitary-d
6	174	100.0	Rat oxytocin secre
7	174	100.0	Rat prolactin-rele
8	174	100.0	19p2 ligand peptid
9	174	100.0	Rat type G protein
10	174	100.0	Rat oxytocin secrete
11	174	100.0	Rat type G protein
12	174	100.0	Rat oxytocin secre
13	174	100.0	Murine pituitary-d
14	174	100.0	Rat type G protein
15	174	100.0	Rat type 11gand po
16	174	100.0	Rat oxytocin secre
17	163	93.7	Bovine G protein-c
18	163	93.7	Bovine pituitary-d
19	163	93.7	Bovine 19p2 ligand
20	163	93.7	Bovine pituitary-d
21	163	93.7	Bovine oxytocin se
22	163	93.7	19p2 ligand peptide
23	163	93.7	Bovine oxytocin se
24	163	93.7	19p2 ligand peptide
25	163	93.7	Bovine oxytocin se
26	163	93.7	Bovine genome-c
27	163	93.7	Bovine pituitary-d
28	163	93.7	Bovine oxytocin se
29	163	93.7	Bovine oxytocin se
30	163	93.7	Bovine oxytocin se
31	163	93.7	Bovine oxytocin se
32	163	93.7	Bovine oxytocin se
33	163	93.7	Bovine oxytocin se
34	163	93.7	Bovine oxytocin se
35	163	93.7	Bovine oxytocin se
36	163	93.7	Bovine oxytocin se
37	163	93.7	Bovine oxytocin se
38	152	87.4	Bovine oxytocin se
39	152	87.4	Bovine oxytocin se
40	149	85.6	Bovine oxytocin se
41	149	85.6	Bovine oxytocin se
42	149	85.6	Bovine oxytocin se
43	149	85.6	Bovine oxytocin se
44	149	85.6	Bovine oxytocin se
45	149	85.6	Bovine oxytocin se

ALIGNMENTS

RESULT ID	1
W31384	W31384 standard; Peptide; 31 AA.
XX	XX
AC	AC
XX	XX
DT	06-APR-1998 (first entry)
XX	XX
DE	Rat type G protein-coupled receptor 1 ligand fragment 1.
XX	G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.
XX	XX
OS	Rat sp.
XX	XX
PN	W09724136-A2.
XX	XX
PD	10-JUL-1997.
XX	XX
PF	26-DEC-1996; 96W0-JP03821.
XX	XX
PR	18-SEP-1996; 96JP-0246573.
PR	28-DEC-1995; 95JP-0243371.
PR	15-MAR-1996; 96JP-0059419.
PR	12-AUG-1996; 96JP-0211805.
XX	XX
(TAKE) TAKEDA CHEM IND LTD.	XX
Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;	XX
PT Kawamata Y, Kitada C;	XX
DR WEP; 1997-363672/33.	XX
N-PSDB; V02421.	XX

XX
 PT ligand peptide for G protein-coupled receptor - acts by modulating
 function in the central nervous system, pancreas and pituitary gland
 XX
 PS Claim 2; Page 179; 258pp; English.

XX
 CC This sequence represents a peptide fragment from a novel rat type
 ligand polypeptide corresponding to amino acid residues 22 to 52 of the
 sequence represented in WO1993 and is used in an assay to monitor ligand
 binding to the G protein-coupled receptor protein. Pharmaceutical
 compositions containing this ligand may be used as a pituitary function
 modulator, a central nervous system modulator or a pancreatic function
 modulator. This ligand could have specific applications as a prophylactic
 or therapeutic agent for dementia, depression, hyperkinetic syndrome,
 disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
 growth hormone secretory disease, hyper- and polyphagia, hyperlipidemia,
 hypercholesterolemia, hyperglyceraemia, diabetes, Turner's syndrome, asthma,
 cancer, pancreatitis, renal disease, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy,
 amyotrophic lateral sclerosis, acute myocardial infarction, infertility,
 CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
 CC osteoporosis and/or oligoagactia. Assays can also be developed to screen
 CC compounds which are capable of altering the binding activity of the
 CC ligand affecting activation of the G protein-coupled receptor protein.
 XX
 Sequence 31 AA:

Query	Match	Score	DB	Length
Best Local Similarity	100.0%	174;	18;	31;
Matches	31; Conservative	Pred. No.	5.8e-19;	
ID	W97233	Mismatches	0;	
XX	standard; Peptide; 31 AA.	Indels	0;	
AC	W97233;	Gaps	0;	
XX				
RESULT	2			
W97233				
XX				
DE	Rat type ligand polypeptide fragment.			
XX				
DR	06-MAY-1999 (first entry)			
XX				
DE	Rat type ligand polypeptide fragment.			
XX				
KW	Rat type ligand; modulation; prolactin secretion;			
KW	G protein-coupled receptor; GPCR; hypogonadism;			
KW	menopausal syndrome; eothyroid; hypometabolism; lactation;			
KW	pituitary adenomatosis; brain tumour; amenorrhea; autoimmune disease;			
KW	prolactinoma; infertility; impotence; amenorrhea; galactorrhea;			
KW	acromegaly; Chiari-I-Frommel syndrome; Argonz-del Castillo syndrome;			
KW	Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;			
KW	contraceptive; Placental function; choriocarcinoma; hydatid mole;			
KW	irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;			
KW	abnormal lipidmetabolism; oxytocia.			
OS	Rattus sp.			
XX				
PN	WO9858962-A1.			
XX				
PD	30-DEC-1998.			
XX				
PF	22-JUN-1998; 98WO-JP02765.			
XX				
PR	23-JUN-1997; 97JP-0165437.			
XX				
PA	(TAKE) TAKEDA CHEM IND LTD.			
XX				
PI	Fuji R, Hinuma S, Kawamata Y, Matsumoto H;			
XX				
DR	WPI; 1999-105614/09.			

Query	Match	Score	DB	Length
Best Local Similarity	100.0%	174;	20;	31;
Matches	31; Conservative	Pred. No.	5.8e-19;	
ID	W87614	Mismatches	0;	
XX	standard; Peptide; 31 AA.	Indels	0;	
AC	W87614;	Gaps	0;	
XX				
RESULT	3			
W87614				
XX				
DE	Rat 19p2 ligand.			
XX				
DR	29-MAR-1999 (first entry)			
XX				
DE	Rat 19p2 ligand.			
XX				
KW	19p2 liand; G protein coupled receptor; pituitary;			
KW	prolactin releasing peptide; rat; dementia; breast cancer;			
KW	therapy.			
XX				
OS	Rattus sp.			
PN	EP887417-A2.			
XX				
PD	30-DEC-1998.			
XX				
PF	25-JUN-1998; 98EP-0111725.			
XX				
PR	27-JUN-1997; 97JP-0172118.			
XX				
PA	(TAKE) TAKEDA CHEM IND LTD.			
XX				
PI	Moriya T, Nishimura O, Suenaga M, Tanaka Y;			
XX				
DR	WPI; 1999-047884/05.			
XX				
PT	Producing a 19p2 pituitary G protein receptor ligand - by cleavage			
PT	of a fusion protein, useful for preventing and treating dementia,			
PT	breast cancer, renal failure and autoimmune disease			
XX				
PS	Claim 5; Page 34; 56pp; English.			

CC This is the amino acid sequence of the rat pituitary G protein-coupled receptor Ligand 19P2L. A method suitable for

CC commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with

CC human basic fibroblast growth factor (see V83794-95) that has been modified to include an N-terminal cysteine residue. The

CC ligand is released from the fusion by cyanylation followed by ammonolysis. 19P2L has prolactin secretion-stimulating and (at

CC high doses) prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including:

CC senile dementia, cerebrovascular dementia, and dementia associated with: neurological disorders (e.g. Alzheimer's disease, Parkinson's

CC disease, Pick's disease, Huntington's disease), infectious diseases (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or

CC toxicosis (e.g. hypothyroidism; vitamin B12 deficiency, alcoholism, intoxication by drugs, metal and organic compounds), tumourigenic diseases (e.g. brain tumour), traumatic diseases (e.g. chronic

CC subarachnoidal hemorrhage), and other types of dementia, depression, hyperactive child syndrome (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hypo and hypersecretion respectively, including: hyperprolactinaemia, pituitary adenoma,

CC breast cancer, infertility, impotence and autoimmune disease (hypersecretion disorders), and seminal vesicle hypoplasia, osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 19P2 polypeptide/amino acid is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.

XX SQ Sequence 31 AA:
Query Match 100.0%; Score 174; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.8e-19; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSMETRTPDINPAWYGRGRPVGRF 31
Db 1 srahqhsmetrtpdinpawytgrgirgvgrf 31

RESULT 4
W95173
ID W95173 standard; peptide; 31 AA.
AC W95173;
DT 10-MAR-1999 (first entry)

XX SQ Sequence 31 AA:
Query Match 100.0%; Score 174; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.8e-19; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSMETRTPDINPAWYGRGRPVGRF 31
Db 1 srahqhsmetrtpdinpawytgrgirgvgrf 31

RESULT 5
W95174
ID W95174 standard; Protein; 31 AA.
AC W95174;
DT 10-MAR-1999 (first entry)
DE Murine pituitary-derived ligand mature polypeptide sequence.
KW Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeldt-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; epitope.

OS Mus sp.
XX WO9849295-A1.
PN XX 05-NOV-1998.
PD XX 27-APR-1998; 98WO-JP01923.
PP XX 28-APR-1997; 97JP-0109974.
PR XX (TAKE) TAKEDA CHEM IND LTD.
PA XX Fukusumi S, Hinuma S;
PT XX

DR WPI; 1999-009423/01.

XX New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening

XX Disclosure: Page 134; 206pp; English.

CC This represents the matured murine pituitary-derived ligand polypeptide sequence. The polypeptide is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat: senile dementia; Alzheimer's, parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; Poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis; epilepsy and many others; also to improve post-operative nutritional status and as a vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide, expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals.

XX SQ Sequence 31 AA:
Query Match 100.0%; Score 174; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.8e-19; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSMETRTPDINPAWYGRGRPVGRF 31
Db 1 srahqhsmetrtpdinpawytgrgirgvgrf 31

RESULT 5
W95174
ID W95174 standard; Protein; 31 AA.
AC W95174;
DT 10-MAR-1999 (first entry)
DE Murine pituitary-derived ligand polypeptide antigenic epitope.
KW Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeldt-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; epitope.

OS Mus sp.
XX WO9849295-A1.

XX 05-NOV-1998.

XX 27-APR-1998; 98WO-JP01923.

XX 28-APR-1997; 97JP-0109974.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Fukusumi S, Hinuma S;

PT XX

XX

DR WPI; 1999-009423/01.

XX

PT New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening

XX

PS Disclosure: Page 26; 206pp; English.

XX

The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UPR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis; epilepsy and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-blinding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. Sequences w95174 to w95178 represent antigenic epitopes which can be used for the preparation of anti-ligand polypeptide antibody.

XX

SQ Sequence 31 AA;

Query Match Best Local Similarity 100.0%; Score 174; DB 20; Length 31; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHOHSMETRPPDINPAWNTGRGIRPVGRF 31

Db 1 srqhqmetsrrtpdinpawytrgirpvgrf 31

RESULT 6

ID B10355 standard; Peptide; 31 AA.

XX

AC B10355;

DT 24-NOV-2000 (first entry)

DR Rat oxytocin secretion promoting peptide SEQ ID NO: 18.

XX

KW Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.

XX

OS Rattus sp.

PN WO200038704-A1.

XX

PD 06-JUL-2000.

XX

PR 22-DEC-1999; 99W0-JP07199.

XX

PR 25-DEC-1998; 98JP-P-0369585.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Matsumoto H, Kitada C, Hinuma S;

XX

DR WPI; 2000-452298/39.

XX

PT Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine

XX

This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of Placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion promoter.

SQ Sequence 31 AA;

Query Match Best Local Similarity 100.0%; Score 174; DB 21; Length 31; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHOHSMETRPPDINPAWNTGRGIRPVGRF 31

Db 1 srqhqmetsrrtpdinpawytrgirpvgrf 31

RESULT 7

ID Y87504 standard; Proteln; 31 AA.

XX

AC Y87504;

XX

DT 18-JUL-2000 (first entry)

XX

DR Rat prolactin-releasing peptide, PRPP.

XX

KW Prolactin-releasing peptide; PRPP; GPR10; G protein-coupled receptor; feeding behavior; food intake; modulation; antagonist; anorectic; obesity; agonist; cachexia.

XX

OS Rattus sp.

XX

FT Key location/qualifiers

FT Modified-site

/note= "C-terminal amide"

XX

PN WO200117641-A1.

XX

PD 30-MAR-2000.

XX

PR 22-SEP-1999; 99W0-US21243.

XX

PR 22-SEP-1998; 98US-0101380.

XX

PR 14-OCT-1998; 98US-0172353.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Stricker-Kongrad A, Gu W;

DR WPI; 2000-303231/26.

XX

PT Identifying modulators of body weight by a combination of a cell-free or cell-based assay to identify modulators of GPR10, followed by an in vivo assay for the compounds effect on e.g. feeding behavior

XX

PS Example 2; Page 61; 82pp; English.

CC modulating body weight. The method comprises cell-free and/or cell-based assays that identify compounds which bind to and/or activate or inhibit the activity of GPR10, a G protein-coupled receptor. These assays are then followed by an *in vivo* assay of the effect of the compound on feeding behaviour, body weight or metabolic rate in a mammal. Proactin-releasing peptide (PRRP; Y875Q4) is a ligand of GPR10. Binding of PRRP to GPR10 stimulates a signal transduction cascade, which results in an increase in food intake. Compounds identified using the method of the invention are useful for the modulation of body weight. Antagonists of GPR10 can be used to treat obesity, while GPR10 agonists can be used to treat cachexia. The present sequence represents rat PRRP.

SQ sequence 31 AA:
 Query Match 100.0%; Score 174; DB 21; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.8e-19; Indels 0; Gaps 0;
 Matches 31; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSMETRTPDPINPAWYGRGIRPVGRF 31
 Db 1 srahqhsmetrtpdpinpawygrgirpvgrf 31

RESULT 8
 Y49292 Y49292 standard; peptide: 31 AA.
 AC Y49292;
 XX
 DT 22-FEB-2000 (first entry)
 DE 19p2 ligand peptide fragment.
 KW pituitary; regulatory mechanism; central nervous system; pancreatic.
 OS Rattus sp.
 XX
 PH Key
 FT Modified-site 31
 /note= "C-terminal amide"
 XX
 PN WO9960112-A1.
 XX
 PD 25-NOV-1999.
 PP 20-MAY-1999; 99WO-JP02650.
 PR 21-MAY-1998; 98JP-0140293.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PT Matsumoto H, Kitada C, Hinuma S;
 DR WPI; 1997-363672/33.
 DR N-PSDB; v02422.
 PT Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
 XX
 PS Claim 2; Page 179; 258pp; English.

XX
 CC This sequence represents a peptide fragment from a novel rat type CC ligand polypeptide corresponding to amino acid residues 22 to 53 of the CC sequence represented in W31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secreting disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglycidaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amyotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligoganglia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.

XX
 CC Sequences Y49290-302 represent peptide fragments of the 19p2 ligand.

SQ sequence 31 AA;
 Query Match 100.0%; Score 174; DB 21; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.8e-19; Indels 0; Gaps 0;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSMETRTPDPINPAWYGRGIRPVGRF 31
 Db 1 srahqhsmetrtpdpinpawygrgirpvgrf 31

RESULT 9
 W31385 W31385 standard; Peptide: 32 AA.
 AC W31385;
 XX
 DT 06-APR-1998 (first entry)
 DE Rat type G protein-coupled receptor ligand fragment 2.
 KW G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; Prophylactic; therapeutic agent.
 KW Rat sp.
 XX
 PN W09724436-A2.
 PD 10-JUL-1997.
 XX
 PF 26-DEC-1996; 96WO-JP03821.
 PR 18-SEP-1996; 96JP-0246573.
 PR 28-DEC-1995; 95JP-0343371.
 PR 15-MAR-1996; 95JP-0059419.
 PR 12-AUG-1996; 95JP-0211805.
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PT Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
 PT Kawamata Y, Kitada C;
 XX
 DR WPI; 1997-363672/33.
 DR N-PSDB; v02422.
 PT Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
 XX
 PS Claim 2; Page 179; 258pp; English.

XX
 CC This sequence represents a peptide fragment from a novel rat type CC ligand polypeptide corresponding to amino acid residues 22 to 53 of the CC sequence represented in W31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secreting disease, hyper- and polyphagia, hyperlipidaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amyotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligoganglia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.

XX
 SQ Sequence 32 AA;

		ID	W31386 standard; Peptide; 33 AA.
		XX	
		AC	W31386;
		XX	
QY	1 SRANQNSMERTTPDINPAWYGRRGRPVGRF 31	DT	06-APR-1998 (first entry)
Db	1 srahqsmetrtppdinpawytgrgirpvgrf 31	DR	Rat type G protein-coupled receptor ligand fragment 3.
RESULT	10	XX	G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.
ID	B10356	OS	Rat sp.
XX		XX	
AC	B10356;	PN	W09724436-A2.
XX		XX	
DT	24-NOV-2000 (first entry)	PD	10-JUL-1997.
XX		XX	
DE	Rat oxytocin secretion promoting peptide SEQ ID NO: 19.	PF	26-DEC-1996; 96WO-JP03821.
XX		XX	
KW	Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.	PR	18-SEP-1996; 96JP-0246573.
KW		PR	28-DEC-1995; 95JP-0343371.
KW		PR	15-MAR-1996; 96JP-0059419.
KW		PR	12-AUG-1996; 96JP-0211805.
OS	Rattus sp.	PA	(TAKE) TAKEDA CHEM IND LTD.
XX		XX	
PN	W0200038704-A1.	PI	Fujii R, Fukushima S, Habata Y, Ninuma S, Hosoya M;
XX		PI	Kawamata Y, Kitada C;
PD	06-JUL-2000.	XX	DR
XX		XX	WPI; 1997-343572/33.
PF	22-DEC-1999; 99WO-JP07199.	PT	Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
XX		XX	
PR	25-DEC-1998; 98JP-0369585.	CC	This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 22 to 54 of the sequence represented in W1383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secreting disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglycaemia, hypoprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amyotrophic lateral sclerosis, acute myocardial infarction, infertility, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion promoter.
PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
XX		CC	
PT	Matsumoto H, Kitada C, Hinuma S;	CC	
XX		CC	
DR	WPI; 2000-452298/39.	CC	
XX		CC	
PT	Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine .	CC	
PT	(TAKE) TAKEDA CHEM IND LTD.	CC	
XX		CC	
PS	06-JUL-2000.	CC	
PI	XX	CC	
XX		CC	
DR	XX	CC	
XX		CC	
PR	22-DEC-1999; 99WO-JP07199.	CC	
XX		CC	
PR	25-DEC-1998; 98JP-0369585.	CC	
XX		CC	
PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
XX		CC	
PT	22-DEC-1999; 99WO-JP07199.	CC	
XX		CC	
PR	25-DEC-1998; 98JP-0369585.	CC	
XX		CC	
PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
XX		CC	
PT	06-JUL-2000.	CC	
XX		CC	
DR	XX	CC	
XX		CC	
PR	22-DEC-1999; 99WO-JP07199.	CC	
XX		CC	
PR	25-DEC-1998; 98JP-0369585.	CC	
XX		CC	
PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
XX		CC	
PS	06-JUL-2000.	CC	
PI	XX	CC	
XX		CC	
DR	XX	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PT	06-JUL-2000.	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PS	06-JUL-2000.	CC	
PI	XX	CC	
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DR	XX	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
PI	XX	CC	
XX		CC	
DR	XX	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PS	06-JUL-2000.	CC	
PI	XX	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
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DR	XX	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
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PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
PI	XX	CC	
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PR	22-DEC-1999; 99WO-JP07199.	CC	
XX		CC	
PR	25-DEC-1998; 98JP-0369585.	CC	
XX		CC	
PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
XX		CC	
PS	06-JUL-2000.	CC	
PI	XX	CC	
XX		CC	
DR	XX	CC	
XX		CC	
PR	22-DEC-1999; 99WO-JP07199.	CC	
XX		CC	
PR	25-DEC-1998; 98JP-0369585.	CC	
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PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
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PS	06-JUL-2000.	CC	
PI	XX	CC	
XX		CC	
DR	XX	CC	
XX		CC	
PR	22-DEC-1999; 99WO-JP07199.	CC	
XX		CC	
PR	25-DEC-1998; 98JP-0369585.	CC	
XX		CC	
PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
XX		CC	
PS	06-JUL-2000.	CC	
PI	XX	CC	
XX		CC	
DR	XX	CC	
XX		CC	
PR	22-DEC-1999; 99WO-JP07199.	CC	
XX		CC	
PR	25-DEC-1998; 98JP-0369585.	CC	
XX		CC	
PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
XX		CC	
PS	06-JUL-2000.	CC	
PI	XX	CC	
XX			

AC	KW	gene therapy; transgenic animal.
XX	XX	
DT	OS	Mus sp.
24-NOV-2000	(first entry)	
DE	XK	
Rat oxytocin secretion promoting peptide SEQ ID NO: 20.		
XX	FH	Key
KW	FT	Location/Qualifiers
Rat; oxytocin secretion promoter; G protein-coupled receptor protein;	peptide	1..20
KW	FT	/note= "signal peptide"
treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;	Protein	21..82
caesarean section; artificial fertilization; galactostasis; goat; pig;	FT	/note= "mature protein"
KW	XK	
veterinary medicine; milk production.	PN	W09849295-A1.
XX	PN	
Rattus sp.	PN	05-NOV-1998.
XX	XX	
PN	PN	98WO-JP019231.
XX	PD	06-JUL-2000.
XX	PR	22-DEC-1999; 99WO-JP0199.
XX	PR	25-DEC-1998; 98JP-0369585.
PA	(TAKE) TAKEDA CHEM IND LTD.	
XX	PI	Matsumoto H, Kitada C, Hinuma S;
PI	XX	
DR	WPI; 2000-452298/39.	
XX	PS	
PS	PS	Physiologically-active polypeptide recognized as ligand by G
PT	PT	protein-coupled receptor protein, for promoting secretion of oxytocin,
PT	PT	as drugs for diseases relating to oxytocin secretion and in veterinary
PT	medicine	-
XX	PS	
PS	PS	disclosure; Page 58, 72pp; Japanese.
XX	CC	This invention describes a novel oxytocin secretion-regulating agent
CC	CC	which contains a ligand peptide or its salt for the G protein-coupled
CC	CC	receptor protein. It is useful in the form of drugs for ameliorating,
CC	CC	preventing and treating diseases relating to oxytocin secretion e.g.
CC	CC	weak pains and atonic bleeding, before and after expulsion of placenta,
CC	CC	uterine recovery failure, caesarean section, stoppage of artificial
CC	CC	fertilization or galactostasis and is also applicable in veterinary
CC	CC	medicine for promoting milk production in cow, goat and pig. This
CC	CC	sequence represents a rat peptide which acts as an oxytocin secretion
CC	CC	promoter.
SQ	Sequence	33 AA:
Query Match	100 %; Score 174; DB 21; Length 33;	
Best Local Similarity	100.0%; Pred. No. 6.2e-19;	
Matches	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 SRRAHQHSMETRDPDINPAWTGGRGIRGVGRF 31	
Db	1 srrahqhsmetrtpdinpawytggrgirgvgrf 31	
RESULT	13	
W95172	ID	W95172 standard; Protein; 82 AA.
XX	AC	
W95172;	AC	
XX	AC	
DE	DE	Murine pituitary-derived ligand polypeptide.
XX	DE	
Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;		
GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;		
tissue; screen; therapeutic; binding; senile dementia; lizard; murine;		
Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;		
Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;		
secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;		
KW		
XX	RESULT	14
XX	W31383	W31383 standard; Protein; 83 AA.
XX	AC	
W31383;	AC	
XX	AC	
DE	DE	Rat type G protein-coupled receptor ligand encoded by PRMV3.

XX G protein-coupled receptor; ligand binding; pharmaceutical;
 KW modulator; pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.
 XX Rat sp.
 XX WO9724436-A2.
 XX PD 10-JUL-1997.
 XX PF 26-DEC-1995; 96WO-JP03821.
 XX PR 18-SEP-1995; 96JP-0246573.
 XX PR 28-DEC-1995; 95JP-0343371.
 XX PR 15-MAR-1996; 96JP-0059419.
 XX PR 12-AUG-1996; 96JP-0211805.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
 XX PI Kawamata Y, Kitada C;
 XX DR WPI; 1997-363672/33.
 DR N-PSDB; V02420.
 XX PT Ligand Peptide for G protein-coupled receptor - acts by modulating
 PT function in the central nervous system, pancreas and pituitary gland
 PS Claim 3; Page 178; 258PP; English.

XX This sequence represents a novel rat type ligand polypeptide encoded by
 CC PRAV3 which is used in an assay to monitor ligand binding to the G
 CC protein-coupled receptor protein. Pharmaceutical compositions
 CC containing this ligand may be used as a pituitary function modulator, a
 central nervous system modulator or a pancreatic function modulator. This
 CC ligand could have specific applications as a prophylactic or therapeutic
 agent for dementia, depression, hypokinetic syndrome, disturbance of
 CC consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone
 secretory disease, hyper- and polyphagia, hypercholesterolemia,
 CC hyperglyceraemia, hyperlipidaemia, hyperprolactinaemia, diabetes,
 cancer, pancreatitis, renal disease, Turner's syndrome, neurorosis,
 CC rheumatoid arthritis, spinal injury, transient brain ischaemia,
 CC amyotrophic lateral sclerosis, acute myocardial infarction,
 CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
 CC osteoporosis, asthma, epilepsy, infertility and/or oligoallactia. Assays
 CC can also be developed to screen compounds which are capable of altering
 CC the binding activity of the ligand thus affecting activation of the G
 CC protein-coupled receptor protein.
 XX Sequence 83 AA;
 SQ

Query Match 100.0%; Score 174; DB 18; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.8e-18; Matches 31; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SRAHQHSMETRIPDINPAWYRGTRPVGR 31
 Db 22 srahqhsmetrtpdinpawyrgtrgvgrf 52

RESULT 15
 ID W97225 Standard; Peptide: 83 AA.
 XX AC W97225;
 XX DT 06-MAY-1999 (first entry)
 XX DE Rat type ligand polypeptide.
 KW G protein-coupled receptor; GPCR; hypogonadism; gonocyst; cacogenes;

XX monopausal syndrome; euthyroid; hypometabolism; lactation; modulation;
 KW pituitary adenomatosis; brain tumour; emmanophobia; autoimmune disease;
 KW prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
 KW acromegaly; Chiari-Fröhmenel syndrome; Argonz-del Castillo syndrome;
 KW Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
 KW contraceptive; placental function; choriocarcinoma; hydatid mole;
 KW irrigation mole; abortion; unthrifly fetus; abnormal saccarometabolism;
 KW abnormal lipidmetabolism; oxytocia; prolactin secretion;
 KW rat type ligand.
 XX OS Rattus sp.
 XX PN WO958962-A1.
 XX PR 30-DEC-1998.
 XX PF 22-JUN-1998; 98WO-JP02765.
 XX PR 23-JUN-1997; 97JP-0165437.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Fujii R, Hinuma S, Kawamata Y, Matsunoto H;
 XX DR WPI; 1999-105614/09.
 XX N-PSDB; X1525.
 XX PT Use of G protein-coupled receptor ligands - for modulating prolactin
 PT secretion or placental function, e.g. for treating menopausal
 PT syndrome, tumours, autoimmune disease or abnormal pregnancy
 XX PS Disclosure; Page 152; 241PP; English.
 CC The present sequence represents a rat type ligand polypeptide. The
 CC specification describes an agent for modulating prolactin secretion
 CC which comprises a ligand polypeptide or a salt, for a G protein-coupled
 CC receptor (GPCR) protein. The agents for promoting prolactin secretion
 CC can be used for treating or preventing hypoparathyroidism, gynecomastia
 CC or aplastic anemia. The agents for promoting lactation in a domestic mammal and as an
 CC aphrodisiac. The agents for inhibiting prolactin secretion can be used
 CC for treating or preventing pituitary adenomatosis, brain tumour,
 CC emmenopathy, autoimmune disease, prolactinoma, infertility, impotence,
 CC amenorrhea, galactorrhea, acromegaly, Chiari-Fröhmenel syndrome, Argonz-del
 CC Castillo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome
 CC or dysospermia. The inhibitory agents can also be used as
 CC contraceptives. The agents for modulating placental function can be used
 CC for treating or preventing choriocarcinoma, hydatid mole, irrigation mole,
 CC abnormal lipidmetabolism or oxytocia.

XX Sequence 83 AA;
 SQ

Query Match 100.0%; Score 174; DB 20; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.8e-18; Matches 31; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SRAHQHSMETRIPDINPAWYRGTRPVGR 31
 Db 22 srahqhsmetrtpdinpawyrgtrgvgrf 52

Search completed: April 17, 2001, 15:38:42
 Job time: 349 sec



OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RA	Petruzziella V., Tiranti V., Fernandez P., Ianna P., Carrozzo R.,
OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	RA	Zerviani M.;
NCBI_TAXID=9606;		RT	"Identification and characterization of human cDNAs specific to BC51, PET112, SC1, COX15, and COX11, five genes involved in the formation
[1]		RT	and function of the mitochondrial respiratory chain.";
SEQUENCE FROM N.A.		RT	Genomics 54:494-504(1998).
RA	Lawlor S.,	RL	[2]
RL	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FROM N.A.
DR		RL	TISSUE=RAIN;
EMBL; AL035608; CAB55682.1; -;		RC	Medline=96207277; PubMed=8619474;
FT		RL	Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
NON_TER 54		RN	"A, double adaptor' method for improved shotgun library
SEQUENCE 54 AA; 6110 MW; E2F3C39FB961A9F CRC64;		RT	construction.,"; Anal. Biochem. 236:107-113(1996).
SQ		RN	[3]
Query Match 45.7%; Score 53; DB 4; Length 54;		RP	SEQUENCE FROM N.A.
Best Local Similarity 50.0%; Pred. No. 0.41;		RC	TISSUE=BRAIN;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;		RX	Medline=97264341; PubMed=9110174;
QY 1 TPDDINPAWYIQRGIRP 16		RA	Iu W., Andersson B., Worley K.C., Muzyz D.M., Ding Y., Liu W.,
Db 18 TPANVPTIWAGSGYYP 33		RA	Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
RESULT 3		RT	"Large-scale concatenation of DNA sequencing.,"; Genome Res. 7:353-358(1997).
ID 060687	PRELIMINARY;	RT	EMBL; AF026849; AD08038.1; -;
AC 060687		DR	INTERPRO; IPRO01939; -.
AC 060687; DT 01-AUG-1998 (TREMBLrel. 07, Created)		DR	PFAM; PF00004; AAH; 1.
DR 01-AUG-1998 (TREMBLrel. 07, Last sequence update)		KW	Hypothetical protein.
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)		SQ	SEQUENCE 419 AA; 47534 MW; 7F0F98BA62F2CB88 CRC64;
DE SUSHI-REPEAT PROTEIN.			
GN SRPUL.			
OS Homo sapiens (Human).		Query Match 42.2%; Score 49; DB 4; Length 419;	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Best Local Similarity 80.0%; Pred. No. 15;	
OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.		Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
NCBI_TAXID=9606;		QY 5 NPARYTGRGI 14	
RN [1]		Db 211 NPWKYTDRGI 220	
SEQUENCE FROM N.A.		RESULT 5	
RA Kuroswawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,		ID 085605	PRELIMINARY;
RA Rakestraaw K.M., Neve C.W., Look T.A.,		AC 085605	PRT; 223 AA.
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.		AC 085605;	DT 01-NOV-1998 (TREMBLrel. 08, Created)
DR EMBL; AF050567; AAC15765.1; -;		DR 01-NOV-1999 (TREMBLrel. 12, Last sequence update)	
DR INTERPRO; IPR000435; -;		DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DR IPR001128; -;		DE EXCINUCLEASE ABC SUBUNIT A (FRAGMENT).	
DR PFAM; PF000084; sushi1; 3.		GN	UVRA.
DR PROSITE; PS00066; CRYPTOCHROME_P450; UNKNOWN_1.		OS	Prevotella albensis.
DR SEQUENCE 465 AA; 52971 MW; 4D752B107FF3EB8 CRC64;		OC	Bacterid; CFB group; Bacteroidaceae; Prevotella.
SQ		NCBI_TAXID=77768;	
Query Match 45.7%; Score 53; DB 4; Length 465;		RN	[1]
Best Local Similarity 50.0%; Pred. No. 4.3;		RP	SEQUENCE OF 9-191 FROM N.A.
Matches 1; Conservative 1; Mismatches 7; Indels 0; Gaps 0;		RC	STRAIN=M384;
QY 1 TPDDINPAWYIQRGIRP 16		RA	Walker N.D., McEwan N.R., Wallace R.J.;
Db 18 TPANVPTIWAGSGYYP 33		RT	"Prevotella albensis putative uvrA gene.,";
RESULT 4		RL	Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
09Y276	PRELIMINARY;	DR	EMBL; AF070930; AAC24131.2; -;
ID 09Y276		DR	INTERPRO; IPR001617; -.
AC 09Y276;		DR	PROSITE; PS00211; ABC-TRANSPORTER; 1.
AC 01-NOV-1999 (TREMBLrel. 12, Created)		KW	ATP-binding; Transport.
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)		FT	NON_TER 1
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)		FT	NON_TER 223 223
DE H-BCS1.		FT	SEQUENCE 223 AA; 24579 MW; 2563BA0B0DC2996C9 CRC64;
GN			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Query Match 41.4%; Score 48; DB 2; Length 223;	
OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.		Best Local Similarity 37.8%; Pred. No. 11;	
OX NCBI_TaxId=9606;		Matches 14; Conservative 1; Mismatches 4; Indels 18; Gaps 2;	
[1]		QY 1 TPDDINPAWY-----RGPRPGRF 20	
SEQUENCE FROM N.A.		Db 57 TPNSNPATYGVFSDIRLFWGLPEAKIRGYKP-GRF 92	
RP			
RC			
RX MEDLINE=99097350; PubMed=9878253;			

RESULT		Best Local Similarity 61.5%; Pred: No. 32; Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Q9M371	PRELIMINARY;	PRT;	790 AA.
ID	09M371	Q9RJKW5	PRELIMINARY;
AC	DT	09RJKW5.	PRT;
DT	01-OCT-2000 (TREMBLrel. 15, Created)	09RJKW5.	940 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	09RJKW5.	940 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	09RJKW5.	940 AA.
DE	HYPOTHETICAL 87.4 KDA PROTEIN.	09RJKW5.	940 AA.
OS	Arabidopsis thaliana (mouse-ear cress),	09RJKW5.	940 AA.
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	09RJKW5.	940 AA.
OC	NCBI_TaxID=3702;	09RJKW5.	940 AA.
OX	[1]	09RJKW5.	940 AA.
RN	SEQUENCE FROM N.A.	09RJKW5.	940 AA.
RA	De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K., Mayer K.F.X., Ouequier F., Salamoutab M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.	09RJKW5.	940 AA.
RL	[2]	09RJKW5.	940 AA.
RN	SEQUENCE FROM N.A.	09RJKW5.	940 AA.
RA	EU Arabidopsis sequencing project; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.	09RJKW5.	940 AA.
KW	EMBL; ALI32955; CAB71037.1; -.	09RJKW5.	940 AA.
DR	HYPOTHETICAL PROTEIN.	09RJKW5.	940 AA.
SQ	SEQUENCE 790 AA; 87375 MW; B222724B75690F30 CRC64;	09RJKW5.	940 AA.
Query Match 41.4%; Score 48; DB 10; Length 790; Best Local Similarity 47.4%; Pred. No. 44; Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;			
QY	2 PDINPAWYTGRGRPVGRF 20	09RJKW5.	940 AA.
Db	366 PPNNPRTYGSRGLQPHGRW 384	09RJKW5.	940 AA.
RESULT 7			
O27142	PRELIMINARY;	PRT;	430 AA.
ID	027142	Q9RJKW5.	PRELIMINARY;
AC	027142;	Q9RJKW5.	PRELIMINARY;
DT	01-JAN-1998 (TREMBLrel. 05, Created)	Q9RJKW5.	PRELIMINARY;
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	Q9RJKW5.	PRELIMINARY;
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	Q9RJKW5.	PRELIMINARY;
DE	CONSERVED PROTEIN.	Q9RJKW5.	PRELIMINARY;
GN	MTH070.	Q9RJKW5.	PRELIMINARY;
OS	Methanobacterium thermoaotrophicum.	Q9RJKW5.	PRELIMINARY;
OC	Archaea: Euryarchaeota; Methanobacteriales: Methanobacteriaceae;	Q9RJKW5.	PRELIMINARY;
OC	Methanobacterium.	Q9RJKW5.	PRELIMINARY;
OX	NCBI_TaxID=2166;	Q9RJKW5.	PRELIMINARY;
RN	[1]	Q9RJKW5.	PRELIMINARY;
SEQUENCE FROM N.A.	STRAIN=DETA_B;	Q9RJKW5.	PRELIMINARY;
RC	STRAIN=DETA_B;	Q9RJKW5.	PRELIMINARY;
RX	MEDLINE=98037514; PubMed=9371463;	Q9RJKW5.	PRELIMINARY;
RA	Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J., Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lunn W., Pothier B., Qu D., Spadato R., Vicare J., Wang Y., Wierzbowki J., Gibson R., Jiwanji N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougal S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoaotrophicum RT deltaH: functional analysis and comparative genomics.", J. Bacteriol. 179:7135-7155 (1997).	Q9RJKW5.	PRELIMINARY;
DR	EMBL; AE000877; AAC85559.1; -.	Q9RJKW5.	PRELIMINARY;
DR	INTERPRO; IPR002510;	Q9RJKW5.	PRELIMINARY;
DR	PFAM; PF01523; Pfam-TID; 1;	Q9RJKW5.	PRELIMINARY;
SQ	SEQUENCE 430 AA; 46062 MW; C4FAE47C111749E6 CRC64;	Q9RJKW5.	PRELIMINARY;
Query Match 40.5%; Score 47; DB 1; Length 430;			
RESULT	9	Q9RJKW5.	PRELIMINARY;
Q9RJKW5	PRELIMINARY;	Q9RJKW5.	PRELIMINARY;
ID	Q9RJKW5	Q9RJKW5.	PRELIMINARY;
AC	Q9RJKW5	Q9RJKW5.	PRELIMINARY;
DT	01-MAY-2000 (TREMBLrel. 13, Created)	Q9RJKW5.	PRELIMINARY;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	Q9RJKW5.	PRELIMINARY;
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	Q9RJKW5.	PRELIMINARY;
DE	HYPOTHETICAL 36.3 KDA PROTEIN.	Q9RJKW5.	PRELIMINARY;
GN	NCBI_TaxID=1902;	Q9RJKW5.	PRELIMINARY;
RN	[1]	Q9RJKW5.	PRELIMINARY;
RP	SEQUENCE FROM N.A.	Q9RJKW5.	PRELIMINARY;
RC	STRAIN=A3(2);	Q9RJKW5.	PRELIMINARY;
RA	Seeger K.J., Harris D.; Streptomyces; Streptomyceaceae; Streptomyces.	Q9RJKW5.	PRELIMINARY;
OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetaceae; Streptomyces; Actinomycetales; Streptomyceaceae; Streptomyces.	Q9RJKW5.	PRELIMINARY;
OX	NCBI_TaxID=1902;	Q9RJKW5.	PRELIMINARY;
RN	[2]	Q9RJKW5.	PRELIMINARY;
RP	SEQUENCE FROM N.A.	Q9RJKW5.	PRELIMINARY;
RC	STRAIN=A3(2);	Q9RJKW5.	PRELIMINARY;
RA	Parkhill J., Barrell B.G., Rajandream M.A.;	Q9RJKW5.	PRELIMINARY;
RL	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.	Q9RJKW5.	PRELIMINARY;
RN	[3]	Q9RJKW5.	PRELIMINARY;
RP	SEQUENCE FROM N.A.	Q9RJKW5.	PRELIMINARY;

RC STRAIN=A3(2);
 RA Redenbach M., Kieser H.M., Denapalite D., Eichner A., Culum J.,
 RA Kinashi H., Bowwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol, Microbial, 21:77-96(1995).;
 DR EMBL; AL21746; CAB57411.;
 KW Hypothetical protein.
 SQ SEQUENCE 333 AA; 36312 MW; 884FF2861837FD76 CRC64;

Query Match 40.1%; Score 46.5; DB 2; Length 333;
 Best Local Similarity 35.5%; Pred. No. 29;
 Matches 11; Conservative 2; Mismatches 7; Indels 11; Gaps 1;
 QY 1 TPPDNPWYI-----GRGIRPVGRF 20
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 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Best Local Similarity 53.3%; Pred. No. 34; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 5;

QY	4 INPAWYTGGRGIRPGV 18	Db	54 LDYWKLARGDAPVG 68
QY	1 TPPDNPWYI-----GRGIRPVGRF 20	Db	19 TPWEEPAWREAGLAIGTEARLAHKGIRGPTGK 49
RESULT 10	09PH76 PRELIMINARY; PRT; 333 AA.	RESULT 11	076383 PRELIMINARY; PRT; 527 AA.
ID 09PH76 AC 076383	ID 076383 AC 076383	ID 076383 AC 076383	ID 076383 AC 076383
DT 01-OCT-2000 (TREMBREL. 15, Last sequence update)	DT 01-OCT-2000 (TREMBREL. 15, Last annotation update)	DT 01-NOV-1998 (TREMBREL. 08, Last sequence update)	DT 01-NOV-1998 (TREMBREL. 14, Last annotation update)
DE HYDROXYBENZOATE OCTAPRENYLTRANSFERASE.	DE HYDROXYBENZOATE OCTAPRENYLTRANSFERASE.	DR C24G6.6 PROTEIN.	DR C24G6.6 PROTEIN.
RA Xylella fastidiosa.	RA Xylella fastidiosa.	RA Caeonhabditis elegans.	RA Caeonhabditis elegans.
OC Rhabditidae; Peioderinae; Caenorhabditidae;	OC Rhabditidae; Peioderinae; Caenorhabditidae;	RA Rhabditidae; Peioderinae; Caenorhabditidae;	RA Rhabditidae; Peioderinae; Caenorhabditidae;
OX NCBI_TAXID=2371;	OX NCBI_TAXID=2371;	RN [1]	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RA MEDLINE=20365717; PubMed=10910347;	RA MEDLINE=9410718; PubMed=2906398;	RA MEDLINE=9410718; PubMed=2906398;	RA MEDLINE=9410718; PubMed=2906398;
RA Simpson R.J.G., Reinach F.C., Arruda P., Abreu F.A., Acecito M., Alvarez L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonacorsi E.D., Bordim S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.R.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Fraga J.S., Franca S.C., Franco M.C., Froehne M., Furian L.R., Garnier M., Goldman G.H., Goodman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Jungueira M.L., Kemper A.L.T.O., Netto L.E.S., Krleger J.B., Kuramae E.B., Lambais M.R., Leite L.G.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madeira A.M.B., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Manck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.A., Nascente M.L.Z., Oliveira M.A., Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Savasa W.A., Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., Terrenzi M.F., Truffi D., Tsai S.M., Tshako M.H., Vallada H., Van Slyk M.A., Verjovska Almeida S., Vettore A.L., Zago M.A., Zatz M., Melanis J., Setubal J.C., RT "The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> .", Nature 406:151-157(2000).	RA Waterston R.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.	RA EMBL; AR06736 AAC19213.1; DR INTERPRO; IPR000205; DR INTERPRO; IPR00237; DR PEPM; PF0193; AMINO oxidase; 1 SEQUENCE 527 AA; 59805 MW; 9FB81FB84437C5CB CRC64;	
RA de Oliveira M.C., de Oliveira R.C., Pamieri D.A., Paris A., RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Savasa W.A., Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., Terrenzi M.F., Truffi D., Tsai S.M., Tshako M.H., Vallada H., Van Slyk M.A., Verjovska Almeida S., Vettore A.L., Zago M.A., Zatz M., Melanis J., Setubal J.C., RT "The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> .", Nature 406:151-157(2000).	RA ID 000050 PRELIMINARY; PRT; 555 AA.	RA ID 000050 PRELIMINARY; PRT; 555 AA.	RA ID 000050 PRELIMINARY; PRT; 555 AA.
RA EMBL; PF01040; UBL1; DR SEQUENCE PS00943; UBL1; UNKNOWN_1; SQ 333 AA; 37931 MW; ECF3F4716C9562B95 CRC64;	RA DR TRANSPOSASE.	RA DR TRANSPOSASE.	RA DR TRANSPOSASE.
Query Match 39.7%; Score 46; DB 5; Length 527; Best Local Similarity 58.3%; Pred. No. 56; Mismatches 3; Indels 0; Gaps 0; Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	Query Match 2 PDPINPANTGGR 13	Query Match 2 PDPINPANTGGR 13	Query Match 2 PDPINPANTGGR 13
RA 070 PNVL3ANVAGRG 381	RA 070 PNVL3ANVAGRG 381	RA 070 PNVL3ANVAGRG 381	RA 070 PNVL3ANVAGRG 381
RESULT 12	000050	RESULT 12	000050
AC 000050	AC 000050	AC 000050	AC 000050
DT 01-JUL-1997 (TREMBREL. 04, Created, Last sequence update)	DT 01-JUL-1997 (TREMBREL. 04, Last annotation update)	DT 01-JUL-1997 (TREMBREL. 04, Last sequence update)	DT 01-JUL-1997 (TREMBREL. 04, Last annotation update)
DR 01-NOV-1998 (TREMBREL. 08, Last sequence update)	DR 01-NOV-1998 (TREMBREL. 08, Last annotation update)	DR 01-NOV-1998 (TREMBREL. 08, Last sequence update)	DR 01-NOV-1998 (TREMBREL. 08, Last annotation update)
DE TRANSPOSASE.	DE TRANSPOSASE.	DE TRANSPOSASE.	DE TRANSPOSASE.

Query Match 39.7%; Score 46; DB 2; Length 333;

OS	Aspergillus awamori.
OC	Eukaryota; Fungi; Ascomycota; Eurotiales; Trichocomaceae;
OC	anamorphic Trichocomaceae; Aspergillus.
OX	NCBI-Taxid=105351;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=DV1143F DERIVED FROM NRRL3112; TRANSPONSON=WADER;
RX	MEDLINE=91156905; PubMed=901286;
RA	Nyssone E., Amuton M., Enfield L., Stubbs J., Dunn-Coleman N.S.;
RT	The transposable element <i>Tanl</i> of <i>Aspergillus niger</i> var. <i>awamori</i> , a new member of the <i>Fotl</i> family.;
RT	Mol. Gen. Genet. 253:50-56(1996).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=UVK143F DERIVED FROM NRRL3112; TRANSPONSON=WADER;
RX	MEDLINE=96207472; PubMed=8625427;
RA	Amuton M., Nyssone E., Stubbs J., Diaz-Torres M.R., Dunn-Coleman N.;
RT	"Identification and cloning of a mobile transposon from <i>Aspergillus niger</i> var. <i>awamori</i> .";
RL	Curr. Genet. 29:468-473(1996).
DR	EMBL: U58046; AAC49623.1; -;
SQ	SEQUENCE 555 AA; 62978 MW; 70904D2BE009BA33 CRC64;
Query Match	39.7%; Score 46; DB 3; Length 555;
Best Local Similarity	57.1%; Pred. No. 60;
Matches	8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY	7 AWYTGRCIREPGP 20
Db	237 AWEGQSIPPWTWF 250
RESULT	13
Q9NE93	PRELIMINARY; PRT: 820 AA.
ID	Q9NE93
AC	Q9NE93;
DT	01-OCT-2000 (TREMBLEI, 15, Created)
DT	01-OCT-2000 (TREMBLEI, 15, Last sequence update)
DT	01-OCT-2000 (TREMBLEI, 15, Last annotation update)
DE	HIPDBI=RETICULIN
GN	HIPDBI=RETICULIN B6.4 KDA PROTEIN.
OS	<i>Leishmania major</i> .
OC	Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX	NCBI-Taxid=5664;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=FRIDELIN;
RA	robben J., Aert R., Volckaert G., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G., Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=FRIDELIN;
RA	Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;"A physical map of the <i>Leishmania major</i> Friedelin genome.";
RN	Genome Res. 8:135-145(1998).
DR	EMBL: AL163492; CAB66699.1; -;
KW	Hypothetical protein.
SQ	SEQUENCE 820 AA; 86388 MW; F4CB0D9FBE666817 CRC64;
Query Match	39.7%; Score 46; DB 5; Length 820;
Best Local Similarity	47.1%; Pred. No. 92;
Matches	8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY	2 PDINPAWYTGRGIRPG 18
Db	406 PTSPALYSQNGSQPLG 422
RESULT	14
Q9V3E5	PRELIMINARY; PRT: 267 AA.
ID	Q9V3E5
AC	Q9V3E5;
DT	01-MAY-2000 (TREMBLEI, 13, Created)
DT	01-MAY-2000 (TREMBLEI, 13, Last sequence update)
DT	01-JUN-2000 (TREMBLEI, 14, Last annotation update)
DE	CG4999 PROTEIN.
GN	CG4999.
OS	<i>Drosophila melanogaster</i> (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
PTerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Dipterae; Drosophilidae; Drosophila.
OX	NCBI-TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Ceinkler S.E., Holt R.A., Evans C.A., Gocayne J.D., Ananatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfieffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.J., Arribi J.F., Agbaria A., Au H.-J., Andrews-Pfleiderer C., Baldwin D., Baliev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borikova D., Botchvaruk M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Geibart W.M., Glasser K., Glodek A., Gong F., Gorreki J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Houston K.A., Howell T.J., Wei M.H., Ihiegwan C., Iraldi M., Kaiush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei J., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskrafi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M., Patazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H., Shue B.C., Sjodin-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirsks R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of <i>Drosophila melanogaster</i> "; Science 287:2185-2195(2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Page-McCaw A.W., Tsang G., Rubin G.M.;"Sequencing <i>Drosophila</i> cDNAs related to tetraspansins.";
RT	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RL	EMBL: AE00353; AFM50354.1; -;
DR	EMBL: AB22004; AFM23828.1; -;
DR	FLYBASE; FB90035336; CG4999.
DR	INTERPRO; IPR00301; -;
DR	PFAM; PF00335; transmembrane4; 1.
DR	PRINTS; PR00259; TMFOUR.
SQ	SEQUENCE 267 AA; 29879 MW; DE91A9B2459BB653 CRC64;
Query Match	38.8%; Score 45; DB 5; Length 267;
Best Local Similarity	46.7%; Pred. No. 38;
Matches	7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DINPANYTGRGIRPV 17
 | : ||| :|| :
 Db 171 DASPARVNGKGNRTI 185

RESULT 15

O9NRB7 PRELIMINARY; PRT: 330 AA.
 ID O9NRB7; AC O9NRB7;
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBrel. 15, Last annotation update)
 DE ADAPTER PROTEIN GRID.
 GN GRID.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NCBI_TaxID:9606;
 OR [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20381669; PubMed=10820259;
 RA Ellis J.H., Ashman C., Burden M.N., Kilpatrick K.E., Morse M.A.,
 RA Hamblin P.A.;
 RT *GRID: a novel Grb-2-related adapter protein that interacts with the
 activated T cell costimulatory receptor CD28.;
 RL J. Immunol. 164:5805-5811(2000).
 DR EMBL; AF236119; AAF60319; 1;
 SQ SEQUENCE 330 AA; 37943 MW; 74F4C8D849B56D55 CRC64;

Query Match 38.8%; Score 45; DB 4; Length 330;
 Best Local Similarity 50.0%; Pred. No. 48;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 5 NPAWYNGRGRGIRPVGRF 20
 ||:||:|| :||
 Db 305 NPSWWNTGRLHNKLGGFF 320

search completed: April 17, 2001, 15:48:08
 Job time: 561 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2001, 15:45:54 ; Search time 70.08 Seconds
(without alignments)
19.613 Million cell updates/sec

Title: US-09-446-543A-50
Perfect score: 116
Sequence: 1 TPDINPAWYGRCIRPVGRF 20
scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 67:
1: Pirl:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	51	44.0	962	H69157 excinuclease ABC chain A - Methanobacterium thermoautotrophicum (strain Delta N)
2	49	42.2	1670	S71551 DNA-directed DNA P
3	48.5	41.8	664	F8376 nucleotide-binding motif A (P-loop)
4	48.5	41.4	790	T47959 hypothetical protein
5	47	40.5	430	B69009 conserved hypothetical
6	47	40.5	453	S18597 tubulin beta chain
7	47	40.5	719	2 S61046 AMP1 protein - yeast
8	47	40.5	940	R03322 excinuclease ABC, C
9	47	40.5	972	A0619 excinuclease ABC
10	46.5	40.1	652	I41522 tetracycline resist Gtb-2 related adap
11	46	39.7	330	JED376 hydroxyphenylacetate oc
12	46	39.7	333	R82852 hypothetical protein
13	46	39.7	943	D64057 excinuclease ABC
14	46	39.7	1	S40887 RVS167 protein - yeast
15	45	38.8	482	T21969 hypothetical protein
16	45	38.8	767	2 probable unr protein
17	45	38.8	798	2 S1210
18	45	38.8	940	I4V2CA excinuclease ABC C
19	45	38.8	953	T76454 excinuclease ABC C
20	45	38.8	965	C02562 excinuclease ABC S
21	44	37.9	105	D81319 hypothetical protein
22	44	37.9	184	T47248 ribosomal protein
23	44	37.9	418	2 F75587 probable glycosylt
24	44	37.9	548	2 T45458 hypothetical protein
25	44	37.9	771	2 C75023 DNA polymerase I P
26	44	37.9	945	2 E83117 excinuclease ABC S
27	44	37.9	952	1 T45550 excinuclease ABC C
28	44	37.9	970	2 S77349 excinuclease ABC C
29	37.9	1014	2 T36031	

ALIGNMENTS

RESULT	Match	Score	Length	DB ID	Description
1	H69157	51	962		excinuclease ABC chain A - Methanobacterium thermoautotrophicum (strain Delta N)
					N;Alternate names: uvrA protein
					N;Contains: excinuclease ABC (EC 3.1.-.-) chain A
					C;Species: Methanobacterium thermoautotrophicum
					C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 12-Nov-1999
					C;Accession: H69157
					R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noeiling, J.; Reeve, J.N.
					J. Bacteriol. 179, 7135-7155, 1997
					N;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: full genome sequence of strain Delta H
					A;Reference number: H69000; MVID:98037514
					A;Accession: H69157
					A;status: preliminary; nucleic acid sequence not shown; translation not shown
					A;Molecule type: DNA
					A;Residues: 1-962 <MTH>
					A;Cross-references: GB:AE000828; GB:AE000666; NID:92621504; PIDN:ABB4949.1; PID:g262
					A;Experimental source: strain Delta H
					C;Genetics:
					A;Gene: MTNA43
					A;Start codon: TTT
					C;Superfamily: excinuclease ABC chain A
					C;Keywords: ATP; DNA binding; DNA repair; duplication; hydrolase; P-loop
					F;38-57/Region: nucleotide-binding motif A (P-loop)
					F;632-915/Region: ATP-binding cassette homology <ABC>
					F;649-656/Region: nucleotide-binding motif A (P-loop)
					Query Match Score 51; DB 2; Length 962;
					Best Local Similarity 40.5%; Pred. No. 9.8; Mismatches 4; Indels 18; Gaps 2;
					Matches 15; Conservative 0;
					QY 1 TPDINPAWYG-----RGIPVGF 20
					Db 704 TPRSNPATYGVTHIRELFAQTPEARKRGYRP-GKF 739
					RESULT 2
					S71551 DNA-directed DNA Polymerase (EC 2.7.7.7) KOD, intein containing precursor - Pyrococcus
					N;Contains: DNA endonuclease (EC 3.1.-.-) PI-I; DNA endonuclease (EC 3.1.-.-) PI-II;
					C;Species: Pyrococcus sp.
					C;Variety: strain KOD1
					C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 20-Apr-2000
					C;Accession: S71551
					R;Kakihara, H.; Takegi, M.; Imanaka, T.
					submitted to the EMBL Data Library, March 1994
					A;Description: Cloning and analysis of the DNA polymerase gene from a new hyperthermo
					A;Reference number: S71551
					A;Accession: S71551

Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy B WYTGIRPV 17
Db 399 WYTGGMMPV 408

RESULT 7

S61056 ARP1 protein - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein D1478; protein YDL167c
C;Species: *Saccharomyces cerevisiae*
C;Date: 15-Feb-1995 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
C;Accession: S61046; S31139; S67119
R;Poli, T.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S61010
A;Accession: S61046
A;Molecule type: DNA
A;Residues: 1-719 <POH>
A;Cross-references: EMBL:267750; NID:91061256; PIDN:CAA91579.1; PID:g1061272
R;Weiner, E.P.; Rao, E.; Brendel, M.
Mol. Gen. Genet. 237, 331-358, 1993
A;Title: Molecular structure and genetic regulation of SFA, a gene responsible for resis-
tance to amphotericin B in *Candida albicans*.
A;Reference number: S31138; MUID:93247548
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-492, N'-494-719 <WEB>
A;Cross-references: EMBL:X68020; NID:9577659; PIDN:CAA48159.1; PID:g288590
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Poli, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67708
A;Accession: S67719
A;Molecule type: DNA
A;Residues: 1-719 <POH>
A;Cross-references: EMBL:274215; NID:91431265; PIDN:CAA98741.1; PID:e253076; PID:g143126
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:NRL1; ARP1
A;Cross-references: MIPS:YDL167c; SGD:S0002326
A;Map position: 4L

RESULT 8

Query Match 40.5%; Score 47; DB 2; Length 719;
Best Local Similarity 58.3%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AWYIGRGIREVG 18
Db 244 SWFTQYGVPGV 255

RESULT 9

A70619 excinuclease ABC chain A - *Mycobacterium tuberculosis* (strain H37RV)
A;Reference number: S31139
A;Accession: A70619
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genomic sequence.
A;Accession: A70619
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-972 <COM>
A;Cross-references: GB:Z85982; GB:ALL23456; NID:93261718; PIDN:CA06633.1; PID:g18389
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: uvrA
C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
C;Keywords: ATP; DNA binding; DNA repair; hydrolase
F:32-39/Region: nucleotide-binding motif A (P-loop)
F:637-920/Domain: ATP-binding cassette homology <ABC>
F:654-661/Region: nucleotide-binding motif A (P-loop)

RESULT 10

Query Match 40.5%; Score 47; DB 2; Length 972;
Best Local Similarity 37.8%; Pred. No. 40;
Matches 14; Conservative 1; Mismatches 4; Indels 18; Gaps 2;

Qy 1 TPDINPAWYG-----RGTRPVGRF 20
Db 709 TPRSPNPATVGFDFKIRTLEAAATEAKVRGQGP-GRF 744

RESULT 11

S11522 tetracycline resistance protein tetB - *Clostridium perfringens*
C;Species: *Clostridium perfringens*
C;Date: 18-Aug-2000 #sequence_revision 15-Sep-2000
C;Accession: A82329
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Charon, D.; Brzustowski, M.D.; Vamathevan, J.; Bass, S.; Qin, B.; Dragoi, I.; Sellers, P.; L.R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 405, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035; MUID:20406833
A;Accession: A82329
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-940 <HEI>
A;Cross-references: GB:AE004127; GB:AE003852; NID:9654808; PIDN:AAF93567.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor

F;11-18/Redlon: nucleotide-binding motif A (P-loop)
F;129-132/Region: Grb-binding NKXD motif

Query Match 40.1%; Score 46.5; DB 1; Length 652;

Best Local Similarity 55.6%; Pred. No. 32; Mismatches 10; Conservative 1; MisMatches 6; Indels 1; Gaps 1;

Qy 3 DINPAWYTGRGIRGVGR 19
Db 445 DLNPFWATVGLIEEPRAGR 462

RESULT 11
JE0376

Grb-2 related adaptor protein 2 - human

C;Species: Homo sapiens (man)

C;Accession: JE0376
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000

R;Oiu, M.; Hua, S.; Agrawal, M.; Li, G.; Cai, J.; Chan, E.; Zhou, H.; Luo, Y.; Liu, M.

Biochem. Biophys. Res. Commun. 25, 433-447, 1998

A;Title: Molecular cloning and expression of human Grap-2, a novel leukocyte-specific sh

A;Reference number: JE0376; MUID:99097254

A;Accession: JE0376
A;Status: preliminary

A;Molecule type: mRNA

A;Cross-references: GB:AF102694; NID:93860192; PIDN:ADD04926.1; PID:93860193

A;Contents: annotation

A;Genes: Xf0068

C;Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 39.7%; Score 46; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 19; Mismatches 8; Conservative 2; MisMatches 5; Indels 0; Gaps 0;

Qy 4 IHPAWYTGRGIRGVGR 18
Db 54 LDPIYWKLARGDPRGV 68

RESULT 13
T33175

hypothetical protein C24G6.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T33175
R;Greco, T.; Bradshaw, H.; Kepler, D.

submitted to the BMBL Data Library, May 1998

A;Description: The sequence of C. elegans cosmid C24G6.

A;Reference number: Z31298

A;Accession: T33175
A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-527 <GRE>

A;Cross-references: EMBL:AF067936; PIDH:MAC19213.1; GSPDB:GN00023; CESP:C24G6.6

A;Experimental source: strain Bristol H2; clone C24G6

C;Genetics:

A;Gene: CESP:C24G6.6

A;Map position: 5

A;Introns: 20/3; 77/1; 129/2; 208/3; 470/2

RESULT 12
H82852

hydroxybenzoate octaprenyltransferase XP00683 [imported] - Xylella fastidiosa (strain 9a5

C;Species: Xylella fastidiosa

C;Accession: H82852
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C;Accession: H82852

R;anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:0365717

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: H82852

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-333 <SM>

A;Cross-references: GB:AB003880; GB:AE003849; HDB:99104830; PIBR:AAF82881.1; GSPDB:GN001

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Heto, E.; Docena, C.; El-Dorry, H.; Facincanl, A.P.; Ferreira, A.J.S.

A;Submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Froim

J.D.; Junqueira, M.L.; Kempfer, J.P.; Krieger, E.E.; Kuramae, E.E.; Laird

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A;Authors: Martins, E.M.P.; Matsukuma, de Oliveira, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyakl, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmeri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsuhako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Contents: annotation

A;Genes: Xf0068

C;Superfamily: 4-hydroxybenzoate octaprenyltransferase

RESULT 14
D64057

excinuclease ABC chain A - Haemophilus influenzae

N;Alternate names: vrrA protein

N;Contains: excision endonuclease ABC (EC 3.1.-.-) chain A

C;Species: Haemophilus influenzae

C;Accession: D64057; JC5157
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weissenbach

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A;Authors: Graham, C.L.; McDaniel, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-943 <PTGR>

A;Cross-references: GB:U32711; GB:L42023; HDB:91573214; PIDH:AAC21915.1; PID:91573215

A;Experimental source: strain Rd KW20

R;de la Morena, M.L.; Hendrixson, D.R.; St. Geme III, J.W.

Gene 17, 23-28, 1995

A;Title: Isolation and characterization of the Haemophilus influenzae vrrA gene.

A;Reference number: JCS157; MUID:97080495

A;Status: preliminary

A;Accession: JC5157

A;Molecule type: DNA

A;Residues: 1-162, 'L' 164-235, 'D' 237-424, 'K' 426-462, 'M' 464-513, 'Q' 515-660, 'T' 662

A;Cross-references: GB:U33877; HID:9144488; PIDN:MAC4592.1; PID:9144489

A;Experimental source: strain N187

C;Genetics:
 A;Gene: ura
 C;Function:
 A;Description: has ATPase and DNA binding activity; involved in DNA repair
 C;Superfamily: excinuclease ABC chain A; AMP-binding cassette homology
 C;Keywords: ATP; DNA binding; DNA repair; duplex; hydrolase; P-loop
 F;31-38/Region: nucleotide-binding motif A (P-loop)
 F;633-907/Region: ATP-binding cassette homology <ABC>
 F;640-647/Region: nucleotide-binding motif A (P-loop)

Query Match 39.7%; Score 46; DB 2; Length 943;
 Best Local Similarity 37.8%; Pred. No. 55;
 Matches 14; Conservative 0; Mismatches 5; Indels 18; Gaps 2;
 QY 1 TPDINPANTG-----RGIRPVGRF 20
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 Db 696 TPNSNPATVIGLTFPIELFAGVPEANARGYVP-GRF 731

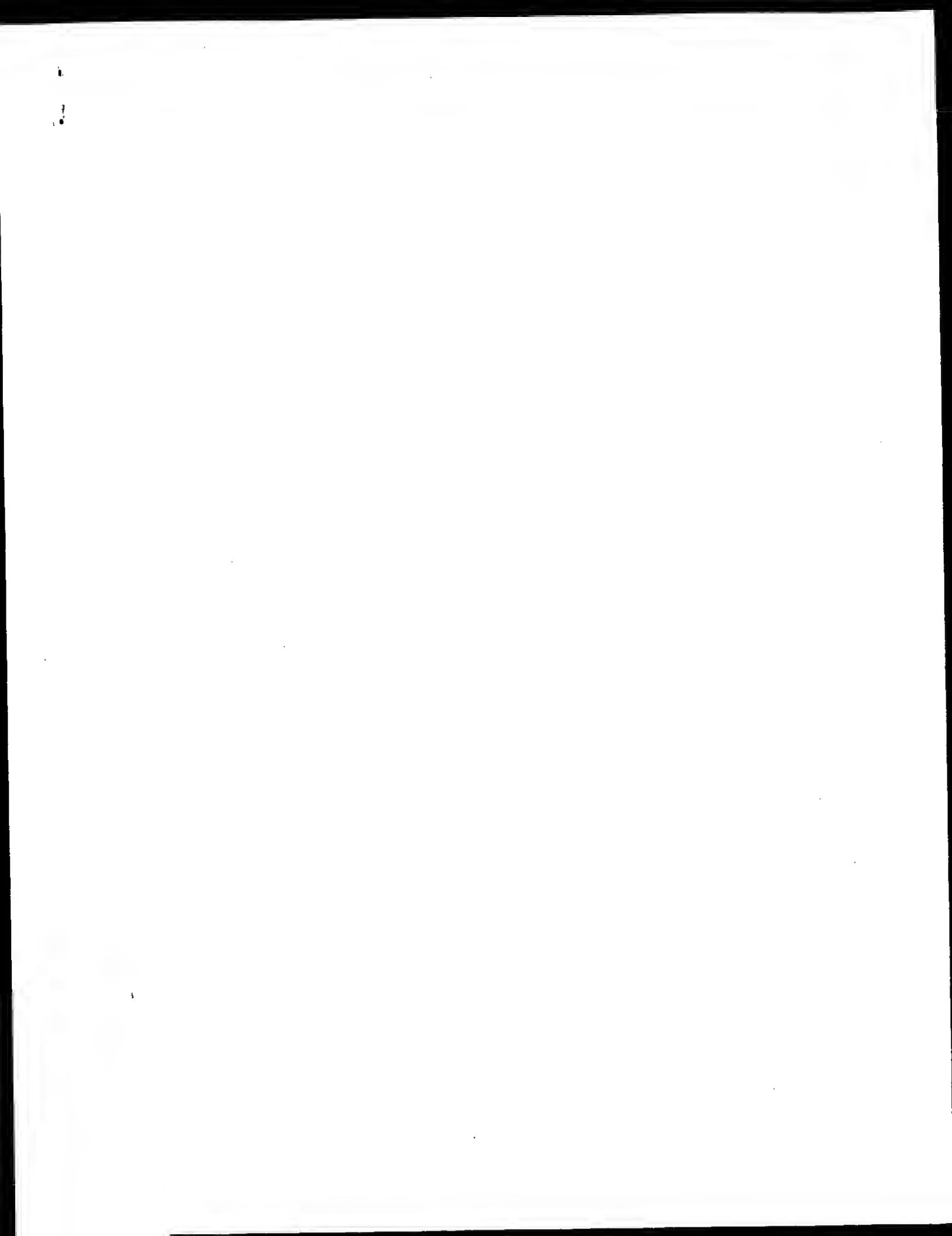
RESULT 15

S40887
 RV3167 protein - yeast (Saccharomyces cerevisiae)
 N;Alternate names: protein YDR88w
 C;Species: Saccharomyces cerevisiae
 C;Date: 31-Mar-1992 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000
 C;Accession: S40887; S69672
 R;Bauer, F.; Urlicci, M.; Aigle, M.; Crouzet, M.
 Mol. Cell. Biol. 13, 507-5084, 1993
 A;Title: Alteration of a yeast SH3 protein leads to conditional viability with defects in
 A;Reference number: S40887; MUID:93330299
 A;Accession: S40887
 A;Molecule type: DNA
 A;Residues: 1-482 <BAU>
 A;Cross-references: EMBL:M92092; NTDB:g172615; PIDN:AAA35051.1; PID:g172616
 R;Dietrich, F.S.
 Submitted to the EMBL Data Library, July 1995
 A;Description: The sequence of S. cerevisiae cosmids 9481, 9509, 9926, 9461, and lambda
 A;Reference number: S69655
 A;Accession: S69672
 A;Molecule type: DNA
 A;Residues: 1-482 <DE>
 A;Cross-references: EMBL:U32274; NID:927313; PIDN:AB64830.1; PID:g927321; GSPDB:GN0000
 C;Genetics:
 A;Gene: SGD:RVS167; MIPS:YDR388w
 A;Cross-references: SGD:S0002796; MIPS:YDR388w
 A;Map position: 4R
 C;Superfamily: RVS167 protein; RVS161 protein homology; SH3 homology
 C;Keywords: transmembrane protein
 F;4-270/Domain: RVS161 protein homology <RVS>
 F;292-422/Region: alanine/glycine/proline-rich
 F;428-477/Region: SH3 homology <SH3>

Query Match 38.8%; Score 45; DB 1; Length 482;
 Best Local Similarity 47.6%; Pred. No. 39;
 Matches 10; Conservative 3; Mismatches 2; Indels 6; Gaps 2;

QY 1 TPDINPANTG-----GIRP 16
 ||| | | | | | : |
 Db 454 TPDSN-ENWIGRYNGQQGFP 473

Search completed: April 17, 2001, 15:45:55
 Job time: 603 sec



GenCore version 4.5
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Om protein - protein search, using sw model

Run on: April 17, 2001, 15:38:42 ; Search time 116.94 Seconds

{without alignments)
9.777 Million cell updates/sec

Title: US-09-446-543A-50
Perfect score: 116
Sequence: 1 TPDINPAWTTGGRGIRPVGRF 20

Scoring table: BLASTm62 Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 5716325 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq-0401:*

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2: /SIDSL1/gcdata/geneseq/geneseq/AA1981.DAT:*

3: /SIDSL1/gcdata/geneseq/geneseq/AA1982.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS			
RESULT	1		
ID	W31387	standard; Peptide: 20 AA.	
XX			
AC	W31387;		
DT	06-APR-1998 (first entry)		
DE	Rat type G protein-coupled receptor ligand fragment 4.		
XX			
KW	G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.		
XX			
OS	Rat sp.		
XX			
PN	W09724436-A2.		
XX			
PD	10-JUL-1997.		
XX			
PF	26-DEC-1996; 96W0-JP03921.		
XX			
PR	18-SEP-1995; 96JP-0246573.		
PR	28-DEC-1995; 95JP-0343371.		
PR	15-MAR-1996; 96JP-0055419.		
PR	12-AUG-1996; 96JP-0211805.		
XX			
PA	{ TAKE } TAKEDA CHEM IND LTD.		
XX			
PI	Fuji R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;		
PI	Kawamura Y, Kitada C;		
XX			
DR	WPI; 1997-363672/33.		
DR	N-PSDB; V02424.		

XX	PT	Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland	PT	Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy	
XX	PS	Claim 2; Page 180; 258pp; English.	PS	Claim 3; Page 154; 241pp; English.	
XX	CC	This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 33 to 52 of the sequence represented in W3183 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglycaidaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amyotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.	CC	The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, or a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypopituitarism, gonostat cacogensis, menopausal syndrome, euthyroid or hypometabolism. They can be used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, eunuchopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome, Forbes-Albright syndrome, Lymphoma, Sheehan syndrome or diszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, interruption mole, abortion, unthrifly fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.	
XX	SQ	Sequence 20 AA;	SQ	Sequence 20 AA;	
Query Match	100.0%	Score 116; DB 18; Length 20;	Query Match	100.0%; Score 116; DB 20; Length 20;	
Best Local Similarity	100.0%	Pred. No. 1.3e-11; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity	100.0%; Pred. No. 1.3e-11; Mismatches 0; Indels 0; Gaps 0;	
Matches	20;	Conservative	Matches	20;	
OY	1	TPDINPAWYTGRGRPVGRF 20	OY	1	TPDINPAWYTGRGRPVGRF 20
Db	1	tpdinpawytgrgrlpvgf 20	Db	1	tpdinpawytgrgrlpvgf 20
RESULT	2	W97234	RESULT	2	W97234 standard; peptide; 20 AA.
ID	W97234		ID	W95175	standard; peptide; 20 AA.
XX			XX		
AC	W97234;		AC	W95175;	
XX			XX		
DT	06-MAY-1999	(first entry).	DT	10-MAR-1999	(first entry)
XX			XX		
DE	Rat type ligand Polypeptide fragment.		DE	Murine pituitary-derived Ligand Polypeptide antigenic epitope.	
XX			XX		
KW	G protein-coupled receptor; GPCR; hypovarianism; gonocyst; cacogenesis; menopausal syndrome; eutrophoid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmenopatism; autoimmune disease; prolactinoma; infertility; impotence; amenorrhoea; galactorrhoea; acromegaly; Chilar-Frommel Syndrome; Argonz del Castilo syndrome; Forbes-Abrilgnt syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; mole; abortion; unfriuity fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.		KW	Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; epitope.	
XX			XX		
OS	Rattus sp.		OS	Mus sp.	
XX			XX		
PN	W09858962-A1.		PN	W0984295-A1.	
XX			XX		
PD	05-NOV-1998.		PD	05-NOV-1998.	
XX			XX		
30-DEC-1998.			PF	27-APR-1998;	98WO-JP01923.
XX			XX		
PF	22-JUN-1998;	98WO-JP02765.	PR	28-APR-1997;	97JP-0109974.
XX			XX		
PR	23-JUN-1997;	97JP-015437.	PA	(TAKE) TAKEDA CHEM IND LTD.	
XX			XX		
PA	(TAKE) TAKEDA CHEM IND LTD.		PA	(TAKE) TAKEDA CHEM IND LTD.	
XX			XX		
PI	Fuji R, Hinuma S, Kawamata Y, Matsumoto H;		PI	Fukusumi S, Hinuma S;	
XX			XX		
DR	WPI; 1999-105614/09.		DR	WPI; 1999-009423/01.	
XX			XX		
PT	New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and		PT		

XX	PS	Disclosure; Page 26; 206pp; English.
CC	CC	The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; creutzfeldt-jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis; epilepsy and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutant are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. Sequences W9514 to W95178 represent antigenic epitopes which can be used for the preparation of anti-ligand polypeptide antibody.
CC	CC	Sequence 20 AA;
CC	CC	SQ
XX	XX	Query Match 100.0%; Score 116; DB 20; Length 20; Best Local Similarity 100.0%; Pred. No. 1_3e-11; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1	TPDINPAWYRGIRGPVGR 20
DB	1	tpdinpawyrgirgpvgrf 20
RESULT 4		
B10358		
ID B10358 standard; peptide: 20 AA.		
XX		
XX		
AC B10358;		
XX		
DR 24-NOV-2000 (first entry)		
XX		
DE Rat oxytocin secretion promoting peptide SEQ ID NO: 21.		
KW Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; uterine bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.		
KW		
OS Rattus sp.		
XX		
PN WO200038704-A1.		
XX		
PD 06-JUL-2000.		
XX		
PF 22-DEC-1999; 99WO-JP07199.		
XX		
PR 25-DEC-1998; 98JP-0369585.		
XX		
PA (TAKE) TAKEDA CHEM IND LTD.		
XX		
PI Matsunoto H, Kitada C, Hinuma S;		
XX		
DR WPI; 2000-452298/39.		
XX		
PT Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary		
PT		

PT	medicine -
PS	Claim 5; Page 58; 72pp; Japanese.
XX	This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion promoter.
CC	sequence represents a rat peptide which acts as an oxytocin secretion promoter.
CC	XX
SQ	Sequence 20 AA;
Query Match	100.0%; Score 116; DB 21; Length 20;
Best Local Similarity	100.0%; Pred. No. 1.3e-11;
Matches 20;	Mismatches 0; Indels 0; Gaps 0;
QY	1 FPDINPAWYGRGDRKRPVGRF 20
XX	
Db	1 tpdlnpawtygrgirgvgrf 20
RESULT	5
ID	Y49302 standard; Peptide: 20 AA.
XX	
AC	Y49302;
XX	
DT	22-FEB-2000 (first entry)
XX	
DE	19P2 ligand peptide fragment.
XX	
KW	Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.
XX	
OS	Rattus sp.
FH	Location/Qualifiers
FT	Modified-site 20 /note= "C-terminal amide"
XX	
PN	W09960112-A1.
XX	
PD	25-NOV-1999.
XX	
PF	20-MAY-1999; 99WO-JP02650.
XX	
PR	21-MAY-1998; 98JP-0140293.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PT	Matsumoto H, Kitada C, Hinuma S;
XX	
DR	WPI; 2000-039381/03.
XX	
PT	New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality
XX	
PS	Disclosure; Page 27; 73pp; Japanese.
XX	
CC	The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative.
CC	

RESULT 8
 ID W31389
 ID W31389 standard; Peptide; 22 AA.
 XX
 AC W31389:
 XX
 DT 06-APR-1998 (first entry)
 DE Rat type G protein-coupled receptor ligand fragment 6.
 KW G protein-coupled receptor; ligand binding; pharmaceutical;
 KW modulator; pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.
 OS Rat sp.
 XX
 PN WO9724436-A2.
 PD 10-JUL-1997.
 XX
 PF 26-DEC-1996; 96WO-JP03821.
 XX
 PR 18-SEP-1996; 96JP-0246573.
 PR 28-DEC-1995; 95JP-0343371.
 PR 15-MAR-1996; 96JP-0059419.
 PR 12-AUG-1996; 96JP-0211805.
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PT Fujii R, Fukushima S, Habata Y, Hinuma S, Hosoya M;
 PI Kawamata Y, Kitada C;
 DR N-PSON; VD2426.
 XX
 PT Ligand peptide for G protein-coupled receptor - acts by modulating
 function in the central nervous system, pancreas and pituitary gland
 XX
 PS Claim 2; Page 181; 258pp; English.
 XX
 CC This sequence represents a peptide fragment from a novel rat type
 peptide corresponding to amino acid residues 33 to 54 of the
 sequence represented in W31383 and is used in an assay to monitor ligand
 binding to the G protein-coupled receptor protein. Pharmaceutical
 compositions containing this ligand may be used as a pituitary function
 modulator, a central nervous system modulator or a pancreatic function
 modulator. This ligand could have specific applications as a prophylactic
 or therapeutic agent for dementia, depression, hypopituitic syndrome,
 growth hormone secretion disease, anxiety syndrome, schizophrenia, trauma,
 hypercholesterolaemia, hyperglycaemia, hypoproactinaemia, diabetes,
 cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma,
 rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy,
 amyotrophic lateral sclerosis, acute myocardial infarction, infertility,
 osteoporosis and/or oligogalactia. Assays can also be developed to screen
 compounds which are capable of altering the binding activity of the
 ligand affecting activation of the G protein-coupled receptor protein.
 XX
 Sequence 22 AA;

Query Match 100.0%; Score 116; DB 18; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.4e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPDINPAWYGRGIRPVGRF 20
 DB 1 tpdinpawytgrgirpvgrf 20

RESULT 9
 ID W31384
 ID W31384 standard; Peptide; 31 AA.
 XX
 AC W31384;
 XX
 DT 06-APR-1998 (first entry)
 DE Rat type G protein-coupled receptor ligand fragment 1.
 XX
 KW G protein-coupled receptor; ligand binding; pharmaceutical;
 KW modulator; pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.

RESULT 10
 ID W31384
 ID W31384 standard; Peptide; 31 AA.
 XX
 AC W31384;
 XX
 DT 06-APR-1998 (first entry)
 DE Rat type G protein-coupled receptor ligand fragment 1.
 XX
 KW G protein-coupled receptor; ligand binding; pharmaceutical;
 KW modulator; pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.

OS	Rat sp.
KW	Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
PN	contraceptive; placental function; choriocarcinoma; hydatid mole;
KW	abnormal lipidmetabolism; oxytocia.
XX	
PD	10-JUL-1997.
XX	
PF	26-DEC-1996; 96WO-JP03821.
XX	
PR	18-SEP-1996; 96JP-0246573.
PR	28-DEC-1995; 95JP-0343371.
PR	15-MAR-1996; 96JP-0059419.
PR	12-AUG-1996; 96JP-0211805.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
P1	Fujii R, Fukushima S, Habata Y, Hinuma S, Hosoya M;
PI	Kawamata Y, Kitada C;
XX	
WPI:	1997-363672/33.
DR	WFPSDB; WO2421.
XX	
PT	Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
XX	
PS	Claim 2; Page 179; 258pp; English.
XX	
CC	This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 22 to 52 of the sequence represented in W31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglycaidaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, transient brain ischaemia, epilepsy, azygoptrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
CC	Sequence 31 AA;
SO	
RESULT	11
W97233	Query Match 100.0%; Score 116; DB 18; Length 31; Best Local Similarity 100.0%; Pred. No. 2.1e-11; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID	W97233 standard; peptide; 31 AA.
XX	
AC	
W97233;	
XX	
DT	05-MAY-1999 (first entry)
DE	Rat type ligand polypeptide fragment.
XX	
KW	Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypovarianism; gonocyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmanipathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome;
KW	
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PR	1999-105614/09.
XX	
PT	Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
XX	
PS	Claim 3; Page 153; 241pp; English.
XX	
CC	The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypoovarianism, gonocyst carcinogenesis, menopausal syndrome, euthyroid or hypometabolism. They can be used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmenopathy, autoimmune disease, proctostomia, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome, Forbes-Albright Syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, eruption mole, abortion, unthrifty fetus, abnormal starcharmetabolism, abnormal lipidmetabolism or oxytocia.
CC	Sequence 31 AA;
SO	
RESULT	12
W8714	Query Match 100.0%; Score 116; DB 20; Length 31; Best Local Similarity 100.0%; Pred. No. 2.1e-11; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID	W8714 standard; peptide; 31 AA.
XX	
AC	
W8714;	
XX	
DT	29-MAR-1999 (first entry)
DE	Rat 19P2 ligand.
XX	
KW	19P2 ligand; G Protein coupled receptor; Pituitary; prolactin releasing peptide; rat; dementia; breast cancer; therapy.
XX	
OS	Rattus sp.
XX	

XX	PR	EP887417-A2.
XX	PD	30-DEC-1998.
XX	PT	25-JUN-1998;
XX	PT	98EP-0111725.
XX	PR	27-JUN-1997;
XX	PR	97JP-0172118.
XX	(TAKE) TAKEDA CHEM IND LTD.	
PT	Moriya T, Nishimura O, Suenaga M, Tanaka Y;	
XX	DR	WPI; 1999-047884/05.
CC	PT	producing a 19P2 pituitary G protein receptor ligand - by cleavage of a fusion protein, useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease
CC	PT	breast cancer, renal failure and autoimmune disease
XX	PS	Claim 5, Page 34; 56pp; English.
XX	CC	This is the amino acid sequence of the rat pituitary G protein-coupled receptor ligand 19P2L. A method suitable for commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see WO94/95) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanation followed by ammonolysis. 19P2L has prolactin secretion-stimulating and (at high doses) prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including: senile dementia, cerebrovascular dementia, and dementia associated with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's disease, Pick's disease, Huntington's disease), infectious diseases (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or intoxicosis (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism, diseases by drugs, metal and organic compounds), tumourigenic subarachnoidal haemorrhage, and other types of dementia, depression, hyperreactive child syndrome (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hypo and hypersecretion respectively, including: hyperprolactinaemia, pituitary adenoma, breast cancer, infertility, impotence and autoimmune disease (hyposecretion disorders), and seminal vesicle hypoplasia, osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 19P2 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactagogue in mammalian farm animals.
XX	PS	Sequence 31 AA;
Query Match	100.0%	Score 116; DB 20; Length 31;
Best Local Similarity	100.0%	Pred. No. 2.1e-11;
Matches	20;	Mismatches 0; Indels 0; Gaps 0;
OY	1	TPDINPAWTGGRIPVGKF 20
D _b	12	tpdinpawtggripvgkf 31
RESULT	13	
ID	W95173	
AC	W95173 standard; peptide; 31 AA.	
DT	10-MAR-1999	(first entry)
DE	Murine pituitary-derived ligand mature polypeptide sequence.	
XX	Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;	
KW	tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal.	
XX	OS	Mus sp.
XX	PN	W09849295-A1.
XX	PD	05-NOV-1998.
XX	PR	27-APR-1998;
XX	PR	98WO-JP01923.
XX	PT	28-APR-1997;
XX	PA	97JP-0109974.
XX	(TAKE) TAREDA CHEM IND LTD.	
PI	Fukusumi S, Hinuma S;	
XX	DR	WPI; 1999-009423/01.
XX	PT	New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
XX	PS	Disclosure; Page 134; 206pp; English.
CC	CC	This represents the matured murine pituitary-derived ligand polypeptide sequence. The polypeptide is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or ORNL1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis; epilepsy and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes for primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy; and to develop transgenic animals.
CC	SQ	Sequence 31 AA;
Query Match	100.0%	Score 116; DB 20; Length 31;
Best Local Similarity	100.0%	Pred. No. 2.1e-11;
Matches	20;	Mismatches 0; Indels 0; Gaps 0;
OY	1	TPDINPAWTGGRIPVGKF 20
D _b	12	tpdinpawtggripvgkf 31
RESULT	14	
ID	W95174	
AC	W95174 standard; Protein; 31 AA.	
DT	10-MAR-1999	(first entry)
DE	Murine pituitary-derived ligand polypeptide antigenic epitope.	
XX	Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;	
KW	tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal.	

XX	KW	GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeldt-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasoconstrictor; gene therapy; transgenic animal; epitope.
OS	KW	Mus sp.
XX	KW	W09849295-A1.
PN	KW	05-NOV-1998.
PD	KW	27-APR-1998; 98WO-JP01923.
XX	KW	28-APR-1997; 97JP-0109974.
PA	KW	(TAKE) TAKEDA CHEM IND LTD.
XX	KW	Fukusumi S, Hinuma S;
XX	KW	DR WPI; 1999-009423/01.
XX	KW	New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
PT	KW	PS Disclosure: Page 26; 206pp; English.
XX	KW	The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat Senile dementia; Alzheimer's or Huntington's disease; Creutzfeldt-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis; epilepsy and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutant are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. Sequences W5174 to W5178 represent antigenic epitopes which can be used for the preparation of anti-ligand polypeptide antibody.
PS	KW	Sequence 31 AA:
SQ	KW	Query Match 100.0%; Score 116; DB 20; Length 31; Best Local Similarity 100.0%; Pred. No. 2.1e-11; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TPPDINPAWYTGREGIRPGRF 20 Db 12 tpdinpawytggrirpgrf 31
RESULT 15	KW	Search completed: April 17, 2001, 15:38:42 Job time: 349 sec
B10355	KW	Query Match 100.0%; Score 116; DB 20; Length 31; Best Local Similarity 100.0%; Pred. No. 2.1e-11; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TPPDINPAWYTGREGIRPGRF 20 Db 12 tpdinpawytggrirpgrf 31
ID	KW	AC B10355;
AC	KW	DT 24-NOV-2000 (first entry)
DE	KW	Rat oxytocin secretion promoting peptide SEQ ID NO: 18.

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OM protein - protein search, using sw model
Run on: April 17, 2001, 15:39:48 ; Search time 61.54 Seconds
(without alignments)

6.243 Million cell updates/sec
US-09-446-543A-50
Title: Perfect score:
Sequence: I TPDIRPAWYGRGIREVGRF 20

Scoring table: BIOSUM2
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing first 45 summaries

Issued Patents Aa: *
1: /cgn2_6/podata/2/1aa/*A_COMB.pep: *
2: /cgn2_6/podata/2/1aa/5B_COMB.pep: *
3: /cgn2_6/podata/2/1aa/6A_COMB.pep: *
4: /cgn2_6/podata/2/1aa/6B_COMB.pep: *
5: /cgn2_6/podata/2/1aa/FC01S_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	116	100.0	20	3 US-09-105-678A-40	Sequence 40, Appli
2	116	100.0	21	3 US-09-105-678A-41	Sequence 41, Appli
3	116	100.0	22	3 US-09-105-678A-42	Sequence 42, Appli
4	116	100.0	31	3 US-09-105-678A-8	Sequence 8, Appli
5	116	100.0	31	3 US-09-105-678A-37	Sequence 37, Appli
6	116	100.0	31	4 US-09-172-353-4	Sequence 4, Appli
7	116	100.0	32	3 US-09-105-678A-38	Sequence 38, Appli
8	116	100.0	33	3 US-09-105-678A-39	Sequence 39, Appli
9	111	95.7	20	3 US-09-105-678A-34	Sequence 34, Appli
10	111	95.7	21	3 US-09-105-678A-35	Sequence 35, Appli
11	111	95.7	22	3 US-09-105-678A-36	Sequence 36, Appli
12	111	95.7	31	3 US-09-105-678A-7	Sequence 7, Appli
13	111	95.7	31	3 US-09-105-678A-31	Sequence 31, Appli
14	111	95.7	32	3 US-09-105-678A-32	Sequence 32, Appli
15	111	95.7	33	3 US-09-105-678A-33	Sequence 33, Appli
16	105	90.5	19	3 US-09-105-678A-30	Sequence 30, Appli
17	105	90.5	20	3 US-09-105-678A-46	Sequence 46, Appli
18	105	90.5	21	3 US-09-105-678A-47	Sequence 47, Appli
19	105	90.5	22	3 US-09-105-678A-48	Sequence 48, Appli
20	105	90.5	31	3 US-09-105-678A-9	Sequence 9, Appli
21	105	90.5	31	3 US-09-105-678A-43	Sequence 43, Appli
22	105	90.5	32	3 US-09-105-678A-44	Sequence 44, Appli
23	105	90.5	33	3 US-09-105-678A-45	Sequence 45, Appli
24	104	89.7	21	3 US-09-105-678A-28	Sequence 28, Appli
25	100	86.2	29	3 US-09-105-678A-29	Sequence 29, Appli
26	50	43.1	349	1 US-08-118-270-71	Sequence 71, Appli
50	43.1				Sequence 320, App

Query Match 100.0%; Score 116; DB 3; Length 20;
Best local Similarity 100.0%; Pred. No. 4.e-12;
Matches 20; Conservative 0; Mismatches 0; Index 0; Gaps 0;

RESULT 2
US-09-105-678A-41
; Sequence 41, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Suenaga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,678A
; FILING DATE: 26-JUN-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 48466-342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,678A
; FILING DATE: 26-JUN-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 48466-342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-105-678A-41
; US-09-105-678A-42
; Query Match 100.0%; Score 116; DB 3; Length 22;
; Best Local Similarity 100.0%; Pred. No. 5.3e-12;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY |||||||
; OY 1 TPDINPAWYIGRGRGIRPVGRF 20
; Db 1 TPDINPAWYIGRGRGIRPVGRF 20
; US-09-105-678A-41
; RESULT 4
; US-09-105-678A-8
; Sequence 8, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Suenaga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,678A
; FILING DATE: 26-JUN-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

us-09-105-678A-8

Query Match 100.0% Score 116; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 7.8e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPDINPAWYTGRGIRPVGRF 20
 Db 12 TPDINPAWYTGRGIRPVGRF 31

RESULT 5

US-09-105-678A-37
 Sequence 37, Application US/09105678A
 Patent No. 610382

GENERAL INFORMATION:

APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

; US-09-105-678A-37

Query Match 100.0% Score 116; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 7.8e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPDINPAWYTGRGIRPVGRF 20
 Db 12 TPDINPAWYTGRGIRPVGRF 31

RESULT 6

US-09-172-353-4
 Sequence 4, Application US/09172353
 Patent No. 6197530

GENERAL INFORMATION:

APPLICANT: Stricker-Kongra, Alain
 APPLICANT: Gu, Wei

TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS

FILE REFERENCE: 07734/02001
 CURRENT APPLICATION NUMBER: US/09/172,353

CURRENT FILING DATE: 1998-10-14
 NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 4

LENGTH: 31
 TYPE: PRT
 ORGANISM: Mus musculus

US-09-172-353-4

Query Match 100.0% Score 116; DB 4; Length 31;

Best Local Similarity 100.0%; Pred. No. 7.8e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPDINPAWYTGRGIRPVGRF 20
 Db 12 TPDINPAWYTGRGIRPVGRF 31

RESULT 7

US-09-105-678A-38
 Sequence 38, Application US/09105678A
 Patent No. 610382

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato
 APPLICANT: Morita, Takeo

APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-6440
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

; US-09-105-678A-37

LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-38

Query Match 100.0%; Score 116; DB 3; Length 32;
 Best Local Similarity 100.0%; Pred. No. 8.1e-12; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY 1 TPDINPAWYTGRCIRPVGRF 20
 Db 12 TPDINPAWYTGRCIRPVGRF 31

RESULT 8

US-09-105-678A-39

; Sequence 34; Application US/09105678A

; Patent No. 6103882

; GENERAL INFORMATION:

; APPLICANT: Sueuaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Tanaka, Yoko

; APPLICANT: Nishimura, Osamu

; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-105-678A-34

US-09-105-678A-35

US-09-105-678A-36

US-09-105-678A-37

US-09-105-678A-38

US-09-105-678A-39

US-09-105-678A-40

US-09-105-678A-41

US-09-105-678A-42

US-09-105-678A-43

US-09-105-678A-44

US-09-105-678A-45

US-09-105-678A-46

US-09-105-678A-47

US-09-105-678A-48

US-09-105-678A-49

US-09-105-678A-50

US-09-105-678A-51

US-09-105-678A-52

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US-09-105-678A-55

US-09-105-678A-56

US-09-105-678A-57

US-09-105-678A-58

US-09-105-678A-59

US-09-105-678A-60

US-09-105-678A-61

US-09-105-678A-62

US-09-105-678A-63

US-09-105-678A-64

US-09-105-678A-65

US-09-105-678A-66

US-09-105-678A-67

US-09-105-678A-68

US-09-105-678A-69

US-09-105-678A-70

US-09-105-678A-71

US-09-105-678A-72

Query Match 100.0%; Score 116; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 8.4e-12; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY 1 TPDINPAWYTGRCIRPVGRF 20
 Db 12 TPDINPAWYTGRCIRPVGRF 31

RESULT 9

NEUTRAL TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 US-09-105-678A-35

RESULT 11
 US-09-105-678A-36
 ; Sequence 36, Application US/09105678A
 ; Patent No. 610382
 ; GENERAL INFORMATION:
 ; APPLICANT: Sueuaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 NEUTRAL TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 US-09-105-678A-7

Query Match 95.7%; Score 111; DB 3; Length 31;
 Best Local Similarity 95.0%; Pred. No. 4.7e-11;
 Matches 19; Conservative 0; Nismatches 1; Indels 0; Gaps 0;

QY 1 TPDINPAWYTGGRGIRPVGRF 20
 Db 1 TPDINPAWYTGGRGIRPVGRF 20

RESULT 12
 US-09-105-678A-7
 ; Sequence 7, Application US/09105678A
 ; Patent No. 610382
 ; GENERAL INFORMATION:
 ; APPLICANT: Sueuaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 NEUTRAL TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 US-09-105-678A-7

Query Match 95.7%; Score 111; DB 3; Length 31;
 Best Local Similarity 95.0%; Pred. No. 4.7e-11;
 Matches 19; Conservative 0; Nismatches 1; Indels 0; Gaps 0;

QY 1 TPDINPAWYTGGRGIRPVGRF 20
 Db 12 TDINPAWYTGGRGIRPVGRF 31

INFORMATION FOR SEQ ID NO: 36:

INFORMATION FOR SEQ ID NO: 36:

RESULT 13
 US-09-105-678A-31
 Sequence 31, Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 ;
 ; APPLICANT: Suenaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-32
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-31
 Query Match 95.7%; Score 111; DB 3; Length 31;
 Best Local Similarity 95.0%; Pred. No. 4.7e-11;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; gaps 0;
 OY 1 TPDINPAWYGGRGPVGFR 20
 Db 12 TPDINPAWYGGRGPVGFR 31
 RESULT 14
 US-09-105-678A-32
 ; Sequence 32, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Suenaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

Tue Apr 17 15:46:15 2001

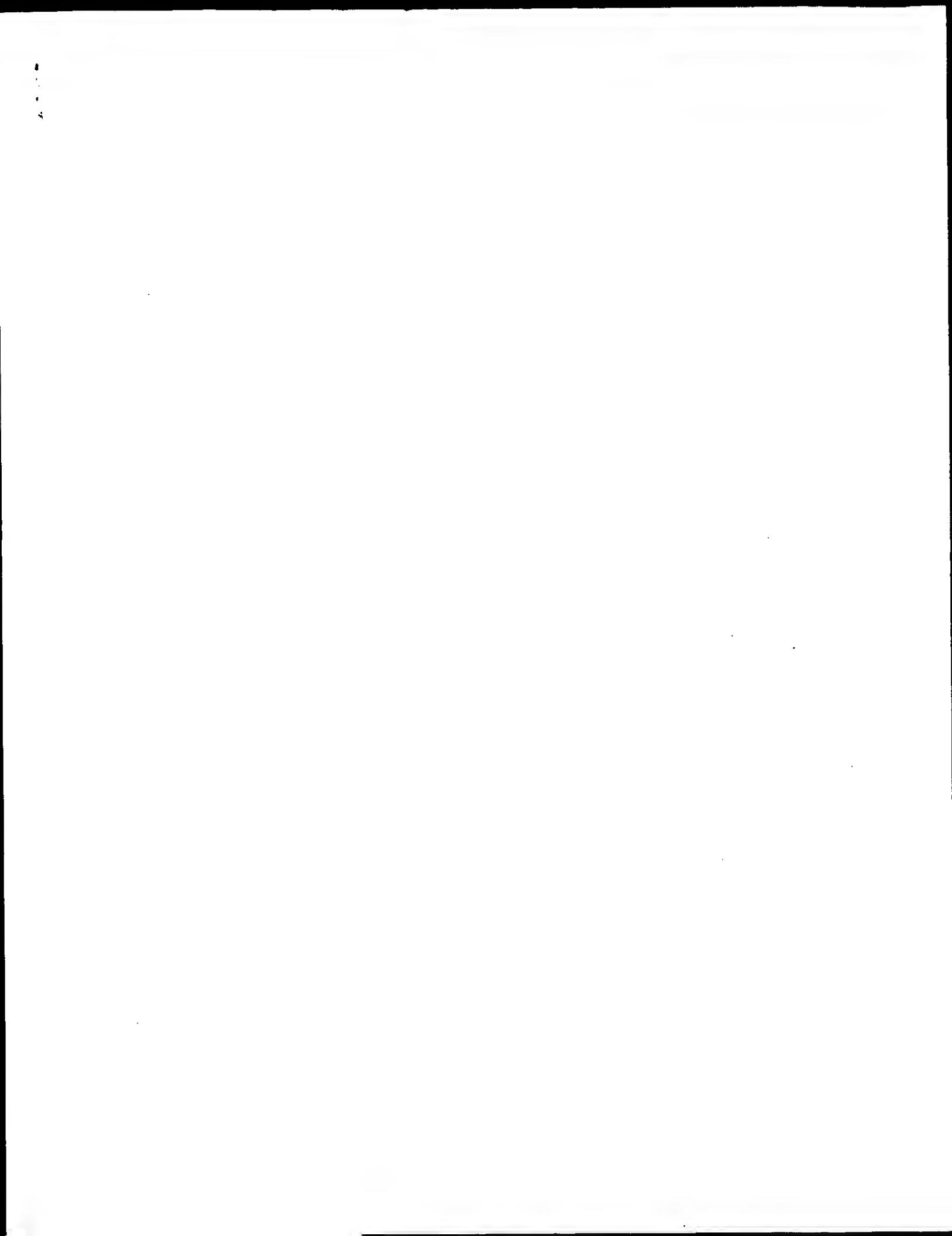
us-09-446-543a-50.ra1

Page 7

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-33

Query Match 95.7%; Score 111; DB 3; Length 33;
Best Local Similarity 95.0%; Pred. No. 5.le-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TPDINPAWYGRGIRPVGRF 20
Db 12 TPDINPAWYGRGIRPVGRF 31

Search completed: April 17, 2001, 15:39:48
Job time: 317 sec



Best Local Similarity 58.3%; Pred. No. 12; Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0; DB 709 TPRSNPATVYGVFDKIRTLFAATPEAKVRYQD-GRF 744

Qy 7 AWTGGRGIRPVG 18
Db 244 SMTQEVRPVG 255

RESULT 7 UVRA_MCYTU STANDARD; PRT: 972 AA.
ID UVRA_MCYTU AC P94972;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE EXCINUCLEASE ABC SUBUNIT A.
GN UVRA OR RV1638 OR MCY05H1.02.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;

RX MEDLINE=98295987; PubMed=9634330;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Nairn D.,
RA Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Telzak F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squires S., Squires R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.", Nature 393:537-544 (1998).

CC -!- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION OF UV DAMAGED NUCLEOTIDE SEGMENTS PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).

CC -!- SUBUNIT: CONSISTS OF THREE SUBUNITS: UVRA, UVRB AND UVRC.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER PROTEIN FAMILY (ABC TRANSPORTERS). CONTAINS TWO ABC DOMAINS

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content IS in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; Z85982; CAB06033.1; -. DR Interpro; IPR001617; -. DR Pfam; PF00005; ABC_tran; 2. DR PROSITE; PS00211; ABC_TRANSPORTER; 2. KW SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat; KW DNA-binding; Zinc-finger.

FT NP_BIND 32 39 ATP (POTENTIAL). FT NP_BIND 654 661 ATP (POTENTIAL). FT ZN_FING 257 285 C4-TYPE (ATYPICAL). FT ZN_FING 753 779 C4-TYPE.

SQ SEQUENCE 972 AA; 106131 MW; 8937A74E592D981 CRC64;

Query Match 40.5%; Score 47; DB 1; Length 972; Best Local Similarity 37.8%; Pred. No. 15; Matches 14; Conservative 1; Mismatches 4; Indels 18; Gaps 2; DB 717 TPSNPNATVYGVFDKIRTLFAATPEAKVRYQD-GRF 752

Qy 1 TPPDINPAWYG-----RGIRPVGRF 20
Db 717 TPSNPNATVYGVFDKIRTLFAATPEAKVRYQD-GRF 752

Qy ~ 1 TPPDINPAWYG-----RGIRPVGRF 20

RESULT	14	OY	1	TPDINPAPYTGRCIRPWRF	20
EX1_HUMAN			:	- : : : :	
ID	EX1_HUMAN	STANDARD;	PRT;	676 AA.	
AC	09235;	AC			
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, last sequence update)			
DT	01-OCT-2000	(Rel. 40, last annotation update)			
DE	EXOSTOSIN-LIKE 1 (EXOSTOSIN-L) (MULTIPLE EXOSTOSIS-LIKE PROTEIN).				
GN	EXT1 OR EXTL				
GN	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.				
OC	NCBI_TaxID=9606;				
OX	OX				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M.; third member				
RT	"Identification and localization of the gene for EXTL, a third member				
RT	of the multiple exostoses gene family";				
RT	Genome Res. 7:10-16(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RT	Xu L., Deng H.X., Xia J.H., Pan Q., Liu C.Y.; mutations of the EXTL genes in hereditary multiple exostoses in Chinese.;				
RT	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Wuyts W., Spieker N., Van Roy N., De Paepe A., De Boulle K., Willemse P.J., Van Hul W., Verstraete R., Speleman F.;				
RA	*Refined physical mapping and genomic structure of the EXTL gene.*;				
RA	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.				
RL	-!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).				
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM (BY SIMILARITY).				
CC	-!- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	U67191; AAC51141.1; -.				
DR	EMBL; AR083633; AAD02840.1; -.				
DR	EMBL; AR083623; AAD02840.1; JOINED.				
DR	EMBL; AR083624; AAD02840.1; JOINED.				
DR	EMBL; AR083625; AAD02840.1; JOINED.				
DR	EMBL; AR083626; AAD02840.1; JOINED.				
DR	EMBL; AR083627; AAD02840.1; JOINED.				
DR	EMBL; AR083628; AAD02840.1; JOINED.				
DR	EMBL; AR083629; AAD02840.1; JOINED.				
DR	EMBL; AR083630; AAD02840.1; JOINED.				
DR	EMBL; AR083631; AAD02840.1; JOINED.				
DR	EMBL; AR083632; AAD02840.1; JOINED.				
DR	EMBL; AR153980; AAF73172.1; -.				
DR	EMBL; AR151391; AAF73172.1; JOINED.				
DR	MIM_501738; -.				
KW	Anti-oncogene; Multigene family; Transmembrane; Signal-anchor.				
FT	TRANSMEM	10	30	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)	
FT	CARBOHYD	269	269	(POTENTIAL).	
FT	SEQUENCE	676 AA;	74673 MN;	N-LINKED (GLCNAc, . .) (POTENTIAL).	
SQ	B5E0008A8762E563 CRC64;				

GenCore version 4.5
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Om protein - protein search, using sw model
Run on: April 17, 2001, 15:48:10 ; Search time 115.07 Seconds
(Without alignments)
20.372 Million cell updates/sec

Title: US-09-446-543A-64
Sequence: 1 TPDINPAWASRGIRVGFR 20

Scoring table: BL2SUM62 Gapext 10.0 , Gapext 0.5

Searched: 37/700 seqs, 117/207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_15;*

- 1: sp_archaea;*
- 2: sp_bacteria;*
- 3: sp_fungi;*
- 4: sp_human;*
- 5: sp_invertebrate;*
- 6: sp_mammal;*
- 7: sp_mhc;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp_rodent;*
- 12: sp_unclassified;*
- 13: sp_vertebrate;*
- 14: sp_virus;*

PRED NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	84	74 3	117	13 09W624 carassius a
2	54	47 8	790	10 09M311 arabidopsis
3	51	45 1	54	4 09uf9 homo sapien
4	51	45 1	465	4 060687 homo sapien
5	47.5	42 0	333	2 09RJ10 streptomyce
6	47	41 6	284	1 050128 pyrococcus
7	47	41 6	333	2 09PH75
8	47	41 6	938	10 09ZVE3 arabiadopsis
9	46.5	41 2	779	3 09P5J9 neurospora
10	46	40 7	1296	5 022452
11	45.5	40 3	1501	10 09SDB6
12	45	39 8	207	5 027455
13	45	39 8	207	5 027455
14	45	39 8	390	2 09PH18
15	45	41 9	419	4 09Y276 homo sapien
16	45	39 8	430	1 027142 methanobact
17	45	39 8	540	10 09LGZ0 oryza sativ
18	45	39 8	767	5 020170 caenorhabdi
19	44.5	39 4	259	2 09LIR4

ALIGNMENTS

RESULT	1
ID	09W624
AC	09W624;
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE	C-RF AMIDE PRCURSOR
OS	Carassius auratus (Goldfish)
RA	Satoko H., Minakata H., Fujimoto M.;
RT	*Carassius RFamide (C-RF amide);
RL	Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL: AB02024; BAM76662; 1. - .;
SQ	SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;

RESULT 1

Query Match Best Local Similarity Score: 84; DB 13; Length 117; Matches 12; Conservative 60.0%; Pred. No. 1.e-05; Mismatches 5; Indels 0; Gaps 0;

QY 1 TPDINPAWASRGIRVGFR 20

Db 56 SPEEDPFVWVGVRPIGRF 75

RESULT 2

09M371 ID 09M371 PRELIMINARY; PRT; 790 AA.

AC 09M371: DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE HYPOTHETICAL 87.4 KDA PROTEIN.

GN 09L616.60

OS Arabidopsis thaliana (Mouse ear cress).

OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	RA	Kurokawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinyro T.,
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;	RA	Rakesstraw K.M., Naeve C.W., Lock T.A.;
OC	Brassicales; Brassicaceae; Arabidopsis.	RL	Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
OX	NCBI_TaxID=3702;	DR	EMBL; AR060567; AAC15655.1; -.
RN	[1]	DR	INTERPRO; IPR000336; -.
RP	SEQUENCE FROM N.A.	DR	INTERPRO; IPR001128; -.
RA	de Haan M., Maarse A.C., Grivell L.A., Newes H.W., Lemcke K.,	DR	PFAM; PF00084; sushi; 3.
RA	Mayer K.F.X., Quetier F., Salanoubat M.;	DR	PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
DR	submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.	DR	SEQUENCE FROM N.A.
RN	[2]	DR	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.
RL	EU_Arabidopsis sequencing project;	DR	SEQUENCE FROM N.A.
RL	Submitted (JAN 2000) to the EMBL/GenBank/DDBJ databases.	DR	SEQUENCE FROM N.A.
DR	EMBL; AL134959; CAB1097.1; -.	DR	SEQUENCE FROM N.A.
KW	Hypothetical Protein.	DR	SEQUENCE FROM N.A.
SQ	SEQUENCE 790 AA; 87375 MW; B22724B75690P30 CRC54;	DR	SEQUENCE FROM N.A.
Query Match	Score 47.8%; DB 10; Length 790;	Query Match	Score 47.8%; DB 4; Length 465;
Best Local Similarity	52.6%; Pred. No. 3.9;	Best Local Similarity	50.0%; Pred. No. 6.4;
Matches	10; Conservative	Matches	8; Conservative
	3; Mismatches		1; Mismatches
	6; Indels		7; Indels
	0; Gaps		0; Gaps
	0;		0;
RESULT	3	RESULT	5
ID	Q9UJF9	ID	Q9RJ0
ID	09UJF9	ID	09RJ0
AC	Q9UJF9;	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, created)	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, last sequence update)	DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	OI-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	DJ47937.3 (SUSHI-REPEAT PROTEIN (SRPUL)) (FRAGMENT).	DE	HYPOTHETICAL 36.3 kDa PROTEIN.
GN	DJ47937.3.	GN	SCF73.05C.
OS	Homo sapiens (Human).	OS	Streptomyces coelicolor.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Actinomycetales; Streptomyceae; Streptomycetaceae; Streptomyces.
OX	NCBI_TaxID=9606;	OX	NCBI_TaxID=1902;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA	Lawlor S.;	RA	Seeger K.J., Harris D.;
RL	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	RL	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AL035608; CAB5682.1; -.	RN	[3]
FT	NON_TER 54	FT	SEQUENCE FROM N.A.
SEQUENCE	54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;	RC	STRAIN=3(2);
RA		RA	Parkhill J., Barrell B.G., Rajandream M.A.;
RL		RL	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR		RN	[3]
FT		RP	SEQUENCE FROM N.A.
SEQUENCE	54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;	RC	STRAIN=3(2);
RA		RA	Reedebach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA		RA	Kinashi H., Hopwood D.A.;
RA		RA	"A set of ordered cosmids and a detailed genetic and physical map for
RT		RI	the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RT		RL	Mol. Microbiol. 21:77-96 (1995).
RT		DR	EMBL; AL121746; CAB57411.1; -.
DE		KW	Hypothetical Protein.
SUSHI-REPEAT PROTEIN.		SQ	SEQUENCE 333 AA; 36312 MW; 884FF2861937FD76 CRC64;
SRPUL.		Query Match	Score 47.5%; DB 2; Length 333;
Homo sapiens (Human).		Best Local Similarity	42.0%; Score 35.5%; Pred. No. 16;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Matches	11; Conservative
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			3; Mismatches
NCBI_TaxID=9606;			6; Indels
[1]			11; Gaps
RP	SEQUENCE FROM N.A.		1;
RESULT	4	RESULT	6
ID	060687	ID	050128
ID	060687	ID	050128
AC	01-AUG-1998 (TREMBLrel. 07, created)	AC	050128;
DT	01-AUG-1998 (TREMBLrel. 07, last sequence update)	DT	01-JUN-1998 (TREMBLrel. 06, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT	01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DE	SUSHI-REPEAT PROTEIN.	DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
GN		DE	HYPOTHETICAL 32.3 kDa PROTEIN PHI420.
OS			
Homo sapiens (Human).			
OC			
OC			
OC			
OX			
OX			
OX			
RN			
RN			
RP			
RESULT	4	Query Match	Score 47.5%; DB 2; Length 333;
ID	060687	Best Local Similarity	42.0%; Score 35.5%; Pred. No. 16;
ID	060687	Matches	11; Conservative
AC	01-AUG-1998 (TREMBLrel. 07, created)		3; Mismatches
DT	01-AUG-1998 (TREMBLrel. 07, last sequence update)		6; Indels
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)		11; Gaps
DE	SUSHI-REPEAT PROTEIN.		1;
SRPUL.			
Homo sapiens (Human).			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID=9606;			
[1]			
RP	SEQUENCE FROM N.A.		
Query Match	Score 47.8%; DB 10; Length 790;	Query Match	Score 47.8%; DB 4; Length 465;
Best Local Similarity	52.6%; Pred. No. 3.9;	Best Local Similarity	50.0%; Pred. No. 6.4;
Matches	10; Conservative	Matches	8; Conservative
	3; Mismatches		1; Mismatches
	6; Indels		7; Indels
	0; Gaps		0; Gaps
	0;		0;
RESULT	3	RESULT	5
ID	Q9UJF9	ID	Q9RJ0
ID	09UJF9	ID	09RJ0
AC	Q9UJF9;	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, created)	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, last sequence update)	DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	OI-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	DJ47937.3 (SUSHI-REPEAT PROTEIN (SRPUL)) (FRAGMENT).	DE	HYPOTHETICAL 36.3 kDa PROTEIN.
GN	DJ47937.3.	GN	SCF73.05C.
OS	Homo sapiens (Human).	OS	Streptomyces coelicolor.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Actinomycetales; Streptomyceae; Streptomycetaceae; Streptomyces.
OX	NCBI_TaxID=9606;	OX	NCBI_TaxID=1902;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA		RA	Seeger K.J., Harris D.;
RL		RL	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR		RN	[3]
FT		RP	SEQUENCE FROM N.A.
SEQUENCE	54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;	RC	STRAIN=3(2);
RA		RA	Parkhill J., Barrell B.G., Rajandream M.A.;
RL		RL	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR		RN	[3]
FT		RP	SEQUENCE FROM N.A.
SEQUENCE	54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;	RC	STRAIN=3(2);
RA		RA	Reedebach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA		RA	Kinashi H., Hopwood D.A.;
RA		RA	"A set of ordered cosmids and a detailed genetic and physical map for
RT		RI	the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RT		RL	Mol. Microbiol. 21:77-96 (1995).
RT		DR	EMBL; AL121746; CAB57411.1; -.
DE		KW	Hypothetical Protein.
SUSHI-REPEAT PROTEIN.		SQ	SEQUENCE 333 AA; 36312 MW; 884FF2861937FD76 CRC64;
SRPUL.		Query Match	Score 47.5%; DB 2; Length 333;
Homo sapiens (Human).		Best Local Similarity	42.0%; Score 35.5%; Pred. No. 16;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Matches	11; Conservative
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			3; Mismatches
NCBI_TaxID=9606;			6; Indels
[1]			11; Gaps
RP	SEQUENCE FROM N.A.		1;
RESULT	4	RESULT	6
ID	060687	ID	050128
ID	060687	ID	050128
AC	01-AUG-1998 (TREMBLrel. 07, created)	AC	050128;
DT	01-AUG-1998 (TREMBLrel. 07, last sequence update)	DT	01-JUN-1998 (TREMBLrel. 06, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT	01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DE	SUSHI-REPEAT PROTEIN.	DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
SRPUL.		DE	HYPOTHETICAL 32.3 kDa PROTEIN PHI420.
Homo sapiens (Human).			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID=9606;			
[1]			
RP	SEQUENCE FROM N.A.		
Query Match	Score 47.8%; DB 10; Length 790;	Query Match	Score 47.8%; DB 4; Length 465;
Best Local Similarity	52.6%; Pred. No. 3.9;	Best Local Similarity	50.0%; Pred. No. 6.4;
Matches	10; Conservative	Matches	8; Conservative
	3; Mismatches		1; Mismatches
	6; Indels		7; Indels
	0; Gaps		0; Gaps
	0;		0;
RESULT	3	RESULT	5
ID	Q9UJF9	ID	Q9RJ0
ID	09UJF9	ID	09RJ0
AC	Q9UJF9;	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, created)	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, last sequence update)	DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	OI-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	DJ47937.3 (SUSHI-REPEAT PROTEIN (SRPUL)) (FRAGMENT).	DE	HYPOTHETICAL 36.3 kDa PROTEIN PHI420.
GN	DJ47937.3.	GN	SCF73.05C.
OS	Homo sapiens (Human).	OS	Streptomyces coelicolor.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Actinomycetales; Streptomyceae; Streptomycetaceae; Streptomyces.
OX	NCBI_TaxID=9606;	OX	NCBI_TaxID=1902;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
Query Match	Score 47.8%; DB 10; Length 790;	Query Match	Score 47.8%; DB 4; Length 465;
Best Local Similarity	52.6%; Pred. No. 3.9;	Best Local Similarity	50.0%; Pred. No. 6.4;
Matches	10; Conservative	Matches	8; Conservative
	3; Mismatches		1; Mismatches
	6; Indels		7; Indels
	0; Gaps		0; Gaps
	0;		0;
RESULT	3	RESULT	5
ID	Q9UJF9	ID	Q9RJ0
ID	09UJF9	ID	09RJ0
AC	Q9UJF9;	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, created)	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, last sequence update)	DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	OI-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	DJ47937.3 (SUSHI-REPEAT PROTEIN (SRPUL)) (FRAGMENT).	DE	HYPOTHETICAL 36.3 kDa PROTEIN PHI420.
GN	DJ47937.3.	GN	SCF73.05C.
OS	Homo sapiens (Human).	OS	Streptomyces coelicolor.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Actinomycetales; Streptomyceae; Streptomycetaceae; Streptomyces.
OX	NCBI_TaxID=9606;	OX	NCBI_TaxID=1902;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
Query Match	Score 47.8%; DB 10; Length 790;	Query Match	Score 47.8%; DB 4; Length 465;
Best Local Similarity	52.6%; Pred. No. 3.9;	Best Local Similarity	50.0%; Pred. No. 6.4;
Matches	10; Conservative	Matches	8; Conservative
	3; Mismatches		1; Mismatches
	6; Indels		7; Indels
	0; Gaps		0; Gaps
	0;		0;
RESULT	3	RESULT	5
ID	Q9UJF9	ID	Q9RJ0
ID	09UJF9	ID	09RJ0
AC	Q9UJF9;	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, created)	AC	09RJ0;
DT	OI-MAY-2000 (TREMBLrel. 13, last sequence update)	DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	OI-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	DJ47937.3 (SUSHI-REPEAT PROTEIN (SRPUL)) (FRAGMENT).	DE	HYPOTHETICAL 36.3 kDa PROTEIN PHI420.
GN	DJ47937.3.	GN	SCF73.05C.
OS	Homo sapiens (Human).	OS	Streptomyces coelicolor.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Actinomycetales; Streptomyceae; Streptomycetaceae; Streptomyces.
OX	NCBI_TaxID=9606;	OX	NCBI_TaxID=1902;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.

GN PH420.
 OS Pyrococcus horikoshi.
 OC Archaea; Eurarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI-TAXID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=c033;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kavarrabiyasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Haga Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Hagai Y.,
 RA Sakai M., Ogura K., Osuka R., Nakawa H., Takamatsu M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kubo Y., Yamazaki J., Kushida H., Oguchi A.,
 Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT *Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshi OT3.;
 RL Res 5.55-761998;
 DR EMBL; AP000006; BAB30526.1; -.
 DR INTERPRO; IPR001066; -.
 DR PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 284 AA; 32319 MW; 8E0E7BC3711D3B15 CRC64;

Query Match 41.6%; Score 47; DB 1; Length 284;
 Best Local Similarity 50.0%; Pred. No. 16; Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0; QY 2 PDIHPAWASRGIRPGVR 19
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:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||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 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshuako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovskii-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Weidman J.J., Setubal J.C.,
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*."
 RL Nature 406:151-157(2000).
 DR EMBL; AE03860; AF2881.1; -.
 DR INTERPRO; IPR00537; -.
 DR PFAM; PF01040; Ubia; 1.
 DR PROSITE; PS00943; Ubia; UNKNOWN_1.
 DR SEQUENCE 333 AA; 37931 MW; ECF3F4716C962B95 CRC64;
 SQ 4 INPAWASRGIRPVG 18
 DB 54 LDPYWLKARGDRPVG 68
 Query Match 41.6%; Score 47; DB 2; Length 333;
 Best Local Similarity 53.3%; Pred. No. 19; Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 4 INPAWASRGIRPVG 18
 DB 23025 PROTEIN.
 SQ Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cV; COLUMBIA;
 RA Rounsey S.D., Lin X., Kaul S., Shea T.P., Fuji C.Y., Mason T.M.,
 RA Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Verner J.C.,
 RT "Arabidopsis thaliana chromosome II BAC TFB8 genomic sequence."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC005561; AAC98465.1; -.
 SQ SEQUENCE 938 AA; 2A4266EGC590B78 CRC64;

Query Match 41.6%; Score 47; DB 10; Length 938;
 Best Local Similarity 66.7%; Pred. No. 56; Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 5 INPAWASRGIRPVG 19
 DB 60 HPAWSASGFIFIGR 74
 SQ 9 O9P5J9 PRO5J9 PRELIMINARY; PRT; 779 AA.
 ID O9P5J9
 AC O9P5J9
 DT 01-OCT-2000 (TREMBLrel. 15. Created)
 DT 01-OCT-2000 (TREMBLrel. 15. Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15. Last annotation update)
 DE RELATED TO BCSC1 PROTEIN PRECURSOR.
 GN B23L21_300.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Sordariales; Sordariaceae; Neurospora.
 RN OX_TAXID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Ryakutina G., Meves H.W., Mannhaupt G.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 SQ [2] Silveira J.F., Silvestri M.L.Z., Siqueira W.J.J., de Souza R.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.H. Jr., de Sa R.G., Santeilli R.V., Savaski H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J.J., de Souza R.A.,

RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL356172; CABE6981; -
 SQ SEQUENCE 779 AA; 85796 MW; CA7891402DEFFBE30 CRC64;

RESULT 10
 Q22452 PRELIMINARY; PRT; 1296 AA.
 ID Q22452;
 AC Q22452;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update)
 DE SIMILAR TO ASGRIN AND FOLLISTATIN.
 GN T13C2.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Plecterinae; Caenorhabditis.
 OX NCBI_TaxID=6329;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulsion A.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawk T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Lateille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Smalton N., Smith K., Sonnhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkison-Sprout J., Wohldman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.",
 RT Nature 338:32-38(1994).
 RN [2] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RN [3] SEQUENCE FROM N.A.
 RA Waterston R.;
 DR Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
 EMBL; U40030: AAA81133.1; -.
 HSSP: P37109; IPI00561; -.
 DR INTERPRO; IPR000561; -.
 DR INTERPRO; IPR001239; -.
 DR INTERPRO; IPR001791; -.
 DR INTERPRO; IPR002049; -.
 DR INTERPRO; IPR002350; -.
 PFAM: PF00050; kazal; 9.
 DR PFAM; PF00053; laminin_EGF; 2.
 DR PRINTS; PRO0220; KAZALINHBT.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS01148; LAMININ_TYPE_EGF; 1.
 SQ SEQUENCE 1296 AA; 145178 MW; 05094BC185839690 CRC64;

Query Match 41.2%; Score 46; DB 3; Length 779;
 Best Local Similarity 58.8%; Pred. No. 55; Gaps 1;
 Matches 10; Conservative 2; MisMatches 2; Indels 3; Gaps 1;

Query Match 1 PRELIMINARY; PRT; 1501 AA.
 ID Q9SD86;
 AC Q9SD86;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE HYPOTHETICAL 164.4 KDA PROTEIN.
 GN F13G24.180.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;

RESULT 11
 Q9SD86 PRELIMINARY; PRT; 1501 AA.
 ID Q9SD86;
 AC Q9SD86;
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 164.4 KDA PROTEIN.
 GN F13G24.180.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;

RESULT 12
 Q9T133 PRELIMINARY; PRT; 153 AA.
 ID Q9T133;
 AC Q9T133;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ENDONUCLEASE.
 GN 3.
 OS Bacteriophage phi-Yeo3-12.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed Phages; Podoviridae;
 OC T7-like phages.
 OX NCBI_TaxID=110457;

RESULT 13
 Q9T133 PRELIMINARY; PRT; 153 AA.
 ID Q9T133;
 AC Q9T133;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ENDONUCLEASE.

SEQUENCE FROM N.A.
 RA Pajunen M.T., Kiljunen S.J., Skurnik M.;
 RT "Complete genomic sequence of the lytic bacteriophage phi-Yeo3-12 of
 Yersinia enterocolitica serotype O:3";
 RT Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AU251805; CAB63604.1; -.
 DR Endonuclease.
 SQ SEQUENCE 153 AA; 17640 MW; 211571BBDE6C641D CRC64;

Query Match 39.8%; Score 45; DB 9; Length 153;
 Best Local Similarity 66.7%; Pred. No. 17; Gaps 0;
 Matches 8; Conservative 2; MisMatches 2; Indels 0; Gaps 0;

QY 9 YASRGIRPVGRF 20
 Best Local Similarity 50.0%; Pred. No. 1.1e-02; Gaps 0;
 Matches 10; Conservative 2; MisMatches 6; Indels 2; Gaps 1;

Db	5 YAARGVKVGAF 16	RA	Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RESULT	13	RA	Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Q2755		RA	Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
ID	Q27455	PRELIMINARY;	Martins E.M.F., Matsukuna A.Y.,
AC	Q27455;	PRT;	Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
DT	01-NOV-1996 (TREMBLrel. 01, Created)	RA	Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	RA	Nhami A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	RA	Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
DE	PHOSPHOENOLPYRUVATE CARBOXYKINASE (EC 4.1.1.32)	RA	Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
DE	(PHOSPHONOLPYRUVATE CARBOXYKINASE (GTp)) (PHOSPHONOLPYRUVATE CARBOXYKINASE (PECK)) (FRAGMENT)	RA	Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
DE	(PHOSPHONOLPYRUVATE CARBOXYKINASE (PECK)) (FRAGMENT)	RA	de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
OC	Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;	RA	da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
OC	Euryptera; Neoptera; Endopterygota; Trichoptera; Integrifalpia;	RA	da Silva J.R., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
OC	Linnophilidae; Brachycentridae; Brachycentrus.	RA	de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Ishaoka M.H.,
OX	[1]	RA	Vallada H., Van Siuys M.A., Verjovskai-Almeida S., Vettore A.L.,
RN	NCBL_TaxID=41036;	RA	Zago M.A., Zatz M., Melani S.J., Setubal J.C.;
RX	SEQUENCE FROM N.A.	RA	"The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> .";
RA	MEDLINE=97036855; PubMed=8882502;	RL	Nature 405:151-157 (2000).
RT	*A nuclear gene for higher level phylogenetics: phosphoenolpyruvate carboxykinase tracks mesozoic-age divergences within Lepidoptera (Insecta).";	DR	EMBL; AE003866; AACB2941.1; -.
RL	Mol. Biol. Evol. 13:594-604 (1996).	DR	INTERPRO: IPR000564; -.
DR	U28445; ARB/362.1; -.	DR	PFAM: PF00821; PECK_1;
DR	PROSITE: PS00505; PECK_GMP; 1.	DR	PFAM: PF00291; PALP; 1.
KW	Pyruvate; Lyase.	DR	INTERPRO: IPR001926; -.
FT	NON_TER 1	DR	SEQUENCE 390 AA; 42479 MW; D294072E6A55188A CRC64;
FT	NON_TER 207	SQ	SEQUENCE 390 AA; 42479 MW; D294072E6A55188A CRC64;
SEQUENCE	207 AA; 22123 MW; 3488D5E4B56B3E8 CRC64;	SQ	SEQUENCE 390 AA; 42479 MW; D294072E6A55188A CRC64;
RESULT	14	Q9Y276	Query Match 39.8%; Score 45; DB 5; Length 207;
Q9PH18	PRELIMINARY; PRT; 390 AA.	ID	Best local similarity 37.0%; Pred. No. 23; Matches 10; Conservative 3; Mismatches 4; Indels 10; Gaps 1;
AC	Q9PH18;	AC	Q9Y276;
DT	01-OCT-2000 (TREMBLrel. 15, Created)	DT	01-NOV-1999 (TREMBLrel. 12, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE	CYSTEINE SYNTHASE.	DE	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
GN	XFO128.	DE	H-BDSL.
OS	xylella fastidiosa.	OS	Homo sapiens (Human).
OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; Xylella; Xylella; Xylella; Xylella; Xylella.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	[1]	OX	NCBL_TaxID=9606;
RN	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	TESSURE-BRAIN;	RC	TESSURE-BRAIN;
RX	MEDLINE=99097350; PubMed=9978253;	RX	MEDLINE=99097350; PubMed=9978253;
RA	Petruzziella V., Tiranti V., Fernandez P., Ianna P., Carrozzo R., Zeviani M.;	RA	Petruzziella V., Tiranti V., Fernandez P., Ianna P., Carrozzo R., Zeviani M.;
RT	Identification and characterization of human cDNAs specific to BCSL, PET112, SCOL, COX15, and COX11, five genes involved in the formation	RT	Identification and characterization of human cDNAs specific to BCSL, PET112, SCOL, COX15, and COX11, five genes involved in the formation
RT	and function of the mitochondrial respiratory chain.;"	RT	and function of the mitochondrial respiratory chain.;"
RL	Genomics 54:494-504 (1998).	RL	Genomics 54:494-504 (1998).
RN	[2]	RN	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.	RC	SEQUENCE FROM N.A.
RX	STRAIN=95SC; MEDLINE=20365117; PubMed=10910347;	RC	TISSUE-BRAIN;
RA	SIMPSON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acecio M., Alvarenga R., Alves L.M.C., Araya J.E., Baita G.S., Baptista C.S., Barros M.H., Bonacorso E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carrasco D.M., Carter H., Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Coste-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Dorena C., El-Dorry H., Fraga J.S., Franca S.C., Franco M.C., Fiolme M., Furian L.R., Gardner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,	RA	Andersson B., Wentland M.A., Ricafrante J.Y., Liu W., Gibbs R.A., "A 'double adaptor' method for improved shotgun library construction.;"
RT	Faccianni A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franca S.C., Franco M.C., Fiolme M., Furian L.R., Gardner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,	RT	Anal. Biochem. 236:107-113 (1996).
RN	[3]	RT	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RC	TISSUE-BRAIN;
RC	MEDLINE=97264341; PubMed=910174;	RX	MEDLINE=97264341; PubMed=910174;
RA	Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W., Riccaffente J.Y., Wentland M.A., Lennon G., Gibbs R.A., "Large-scale concatenation of cDNA sequencing.;"	RA	Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W., Riccaffente J.Y., Wentland M.A., Lennon G., Gibbs R.A., "Large-scale concatenation of cDNA sequencing.;"
RT	Genome Res. 7:353-356 (1997).	RT	Genome Res. 7:353-356 (1997).
RL	EMBL; AF026849; ADD08638.1; -.	RL	EMBL; AF026849; ADD08638.1; -.

DR
EMBL; AF038195; AAB97365.1; -.
DR
INTERPRO; IPR001939; -.
DR
PFAM; PF00004; AAA; 1.
KW
Hypothetical protein.
SQ
SEQUENCE 419 AA; 47534 MW; 7F0E98BA62F2CBB8 CRC64:

Query Match 39.8%; Score 45; DB 4; Length 419;
Best Local Similarity 70.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5 NPAWIASRG1 14
| | | | |
Db 211 NPFWYTDRC1 220

Search completed: April 17, 2001, 15:48:11
Job time: 564 sec

Query Match	44.7%	Score	50.5;	DB	2;	Length	664;
Best Local Similarity	62.5%	Pred. No.	5.5;				
Matches	10;	Conservative	1;	Mismatches	4;	Indels	1;
Qy	1	TPDINPAWASRGIRGP 16					
Db	478	TPDINP-WFLQRSGRP 492					
RESULT	3						
F71015		hypothetical protein PH1420 - Pyrococcus horikoshii					
C;Species:	Pyrococcus horikoshii						
C;Date:	14-Aug-1998	#sequence_revision	14-Aug-1998	#text_change	20-Jun-2000		
C;Accession:	F71015						
R;Kawarabayashi, Y.; Sawada, N.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, N.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, M.; Oguchi, DNA Res. 5: 55-76, 1998							
A;Title:	Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, Pyrococcus horikoshii						
A;Reference number:	A71000; MNUID:98344137						
A;Accession:	F71015						
A;Status:	preliminary; nucleic acid sequence not shown; translation not shown						
A;Molecule type:	DNA						
A;Residues:	1-984 <RAW>						
A;Cross-references:	GB:AB000006; NID:93236133; PIDN:BA30526.1; PID:g3257843						
A;Experimental source:	strain OR3						
A;Note:	this accession replaces an interim accession for a sequence replaced by GenBank						
C;Genetics:							
A;Gene:	PH1420						
C;Superfamily:	Pyrococcus horikoshii hypothetical protein PH1420						
Query Match	41.6%	Score	47;	DB	2;	Length	284;
Best Local Similarity	50.0%	Pred. No.	8;				
Matches	9;	Conservative	3;	Mismatches			
Qy	2	PDINPAWASRGIRGP 19					
Db	217	PYIEPFYALRGLELIGR 234					
RESULT	4						
H82852		hydroxybenzoate octaprenyltransferase XF0068 [imported] - Xylella fastidiosa (strain 9a5					
C;Species:	Xylella fastidiosa						
C;Date:	18-Aug-2000	#sequence_revision	20-Aug-2000	#text_change	17-Nov-2000		
C;Accession:	H82852						
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis							
A;Title:	The genome sequence of the plant pathogen Xylella fastidiosa.						
A;Reference number:	A8215; MNUID:2036517						
A;Accession:	H82852						
A;Status:	preliminary						
A;Molecule type:	DNA						
A;Residues:	1-333 <SIM>						
A;Cross-references:	GB:AB003860; GB:AE003849; NID:99104830; PIDN:AAF82881.1; GSPDB:GN001						
A;Experimental source:	strain 9a5c						
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, N.; Alvarenga, R.; Britolles, M.R.S.; Bueno, N.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.N.; Carrer, E; as-Nero, E.; Docena, C.; El-Borry, H.; Facincani, A.P.; Ferreira, A.J.S.							
A;Authors:	Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Rohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laior, Mado, M.A.; Madeira, A.N.B.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E; Adado, M.; Martins, E.M.F.; Matsuoka, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Martins, E.M.F.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, C.R.; da Silva, F.R.; da Silva, A.N.; Silva Jr., W.A.; da Silveira M.; Tsuhako, N.H.; Valleda, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Genbank:						
C;Genetics:							
Query Match	40.7%	Score	46;	DB	2;	Length	1296;
Best Local Similarity	50.0%	Pred. No.	54;				
Matches	10;	Conservative	2;	Mismatches	6;	Indels	2;
Qy	1	TPDINPAWASRGIRGP 20					
Db	975	TIDINSDNYFSR--KDINRF 992					
RESULT	7						

A;Gene: XF0068
C;Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

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Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

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Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

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Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

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41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

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41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

Query Match

41.6%; Score 47; DB 2; Length 333;

Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 4; Indels 0; Gaps 0;

A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A;Reference number: A70500; MUID:98295987

A;Accession: D70817

A;Status: Preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-276 <CDS>

A;Cross-references: GB:AL022003; GB:ALL23456; NID:93261547; PIDN:CAA17613.1; PID:g326154

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv1716

Query Match 38.9%; Score 44; DB 2; Length 276;
Best Local Similarity 20.0%; Pred. No. 23; Indels 32; Gaps 1;
Matches 10; Conservative 5; Mismatches 3; Indels 32; Gaps 1;

QY 1 PDDINPA-----WASRGTRPVG 18
Db 111 TPDIPRGDIVVNTGWHKYADSAEVAYASPGFDKKGAEWAFAKGVKAVG 160

RESULT 12
A75117 hypothetical protein PAB0502 - *Pyrococcus abyssi* (strain Orsay)
C;Species: *Pyrococcus abyssi*

C;Accession: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

R;anonymous Genoscope

submitted to the EMBL Data Library, July 1999
A;Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome struc-

A;Reference number: A75001

A;Accession: A75117

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-284 <RAW>

A;Cross-references: GB:AJ248285; GB:AL026836; NID:95478067; PIDN:CAB49650.1; PID:g345816

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB0502

C;Superfamily: *Pyrococcus horikoshii* hypothetical protein PH1420

Query Match 38.9%; Score 44; DB 2; Length 284;
Best Local Similarity 44.4%; Pred. No. 23; Mismatches 8; Indels 6; Gaps 0;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 PDINPAWASRGTRPVGR 19
Db 217 PYIEPPTFVALRGELLGK 234

RESULT 13
B70631 hypothetical protein Rv0428c - *Mycobacterium tuberculosis* (strain H37RV)

C;Species: *Mycobacterium tuberculosis*

C;Accession: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

R;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

R;Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skilton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A;Reference number: A70500; MUID:98295987

A;Status: Preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-102 <CDS>

A;Cross-references: GB:Z04724; GB:ALL23456; NID:93261708; PIDN:CAA06568.1; PID:g1817694

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv0428c

C;Superfamily: *Mycobacterium tuberculosis* hypothetical protein Rv0428c

Query Match 38.9%; Score 44; DB 2; Length 302;

Best Local Similarity 30.0%; Pred. No. 25; Indels 1; Gaps 0;

Matches 7; Conservative 2; Mismatches 2;

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-309 <RAW>

A;Cross-references: EMBL:AF025462; PIDN:AA871002.1; GSPDB:GN00021; CESP:K10F12.4

A;Experimental source: strain Bristol N2; cione k10f12

C;Genetics:

A;Gene: CESP:K10F12.4

A;Map Position: 31/3; 123/2; 196/3; 239/1

A;Introns: 31/3; 123/2; 196/3; 239/1

Query Match 38.9%; Score 44; DB 2; Length 309;

Best Local Similarity 44.4%; Pred. No. 25; Indels 5; Gaps 1;

Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-309 <RAW>

A;Cross-references: EMBL:AE002320; GB:AE002160; NID:97190551; PIDN:AAF39360.1; PID:g719

A;Experimental source: strain N199 (MoPrn)

C;Genetics:

A;Gene: TC059

C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology

Query Match 38.9%; Score 44; DB 2; Length 428;

Best Local Similarity 37.5%; Pred. No. 36; Indels 0; Gaps 0;

Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 PDINPAWASRGTRPV 17
Db 196 PDVNPGSYVEESLSP 211

TUE APR 17 15:46:21 2001

us-09-446-543a-64.rpr

Page 5

Search completed: April 17, 2001, 15:45:58
Job time: 606 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on : April 17, 2001, 15:48:51 ; Search time 39.1 Seconds

(without alignments)
17.522 Million cell updates/sec

Title: US-09-446-543a-64

Perfect score: 113

Sequence: 1 TPDINPAWYASRGIRPVGRF 20

Scoring table: BLOSUM62

Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	100.0	87	1 PRRP_HUMAN	P81277 homo sapien
2	109	96.5	98	1 PRRP_BOVINE	P81264 bos taurus
3	105	92.9	83	1 PRRP_RAT	P81278 rattus norvegicus
4	47	41.6	67	1 EXLI_HUMAN	P82935 homo sapien
5	45	41.6	67	1 CYCR_CNRVI	P82947 chromatinium
6	44	38.9	476	1 YAJV_ECOLI	P10143 escherichia
7	44	38.9	719	1 ARP_YEAST	P32770 saccharomyces
8	43.5	38.5	860	1 VGP2_BPB03	P38893 bacteriophaga
9	43	38.1	376	1 OPSL_LIMPO	P53360 limulus polpiger
10	43	38.1	376	1 OPS2_LIMPO	P53361 limulus polpiger
11	42	37.2	332	1 LYTB_WYCLE	Q9X781 mycobacterium
12	42	37.2	364	1 YAWI_ECOLI	P77562 escherichia
13	42	37.2	546	1 CHOD_STRSQ	P12675 streptomyces
14	42	37.2	581	1 POL_MVVK	P31795 radiation
15	42	37.2	843	1 POL_MVAK	P03357 akir murine
16	42	37.2	1196	1 POL_MVRD	P03356 akv murine
17	42	37.2	1196	1 UBLB_RICPR	P11227 radiation
18	41.5	36.7	265	1 UBIE_RICPR	Q9CPC3 rickettsia
19	41	35.3	149	1 ENRN_BPT7	P00641 bacteriophaga
20	41	36.3	342	1 Y762_METJA	Q58172 methanococcus
21	41	36.3	347	1 Y576_METJA	Q57996 methanococcus
22	41	36.3	379	1 YX11_ANASP	P22978 arabacia punicea
23	41	36.3	622	1 PCCC_RAT	P07379 ratetus norvegicus
24	41	36.3	986	1 CYGR_ARBU	P11528 arabacia punicea
25	40.5	35.8	751	1 PR26_RAT	P97750 ratetus norvegicus
26	40	35.4	158	1 RIL15_AERPE	P99798 aeropyrum peruvianum
27	40	35.4	181	1 YK69_CAEEL	P34347 caenorhabditis
28	40	35.4	424	1 SAMB_SALTY	P28832 salmonella
29	40	35.4	556	1 DPOL_WHVW6	P11292 woodchuck hepatitis
30	40	35.4	580	1 ATPU YEAST	P22136 saccharomyces cerevisiae
31	40	35.4	625	1 DHGL_DROME	P19173 drosophila melanogaster
32	40	35.4	746	1 EXTL_HUMAN	P06394 homo sapiens
33	40	35.4	746	1 EXTL_MOUSE	P97464 mus musculus

ALIGNMENTS

34 40 35.4 788 1 RGC2_HAEMIN
35 40 35.4 792 1 STFB_XLFA
35 40 35.4 879 1 DPOL_WIVI
37 40 35.4 884 1 DPOL_WIV59
38 40 35.4 884 1 DPOL_WIV7
39 40 35.4 962 1 UYRA_MEPHTH
40 40 35.4 973 1 UYRA_RHIME
41 40 35.4 987 1 EPB4_MOUSE
42 39.5 35.0 831 1 DPOL_THRELF
43 39.5 35.0 1122 1 TERT_MOUSE
44 39.5 35.0 1882 1 Y468_MCPN
45 39 34.5 61 1 YLCE_ECOLI

P44108 haemophilus ducreyi

Q9Psf_xylella fastidiosa

P03160 woodchuck hepatitis

P12899 woodchuck hepatitis

P12898 woodchuck hepatitis

O26543 methanobacter

P56999 rhizobium meliloti

P54761 mus musculus

P30313 thermus aquaticus

O70372 mus musculus

P75109 mycoplasma pneumoniae

P77087 escherichia coli

RESULT 2

PRRP_BOVIN STANDARD; PRT; 98 AA.

ID PRRP_BOVIN STANDARD; PRT; 98 AA.

AC P81264;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE PROLACTIN-RELEASING PEPTIDE PRECURSOR (PRRP) (PROLACTIN-RELEASING HORMONE) [CONTAINS: PROLACTIN-RELEASING PEPTIDE PRRP31; PROLACTIN-RELEASING PEPTIDE PRRP20].

GN PRH.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovine; Bos.

OC NCBI_TAXID=9913;

RN [1] SEQUENCE FROM M.A., AND SEQUENCE OF 23-52.

RC TISSUE-BRAIN;

RX MEDLINE=98268781; PubMed=9607765;

RA Hinuma S., Rabata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitaeda C., Nasuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.

RT "A prolactin-releasing peptide in the brain." Nature 393:272-276 (1998).

RL -!- FUNCTION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.

CC -!- TISSUE SPECIFICITY: MEULLA OBLONGATA AND HYPOTHALAMUS.

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CC DR Hormone; Amidation; Signal; Cleavage on pair of basic residues.

CC RA Hinuma S., Rabata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitaeda C., Nasuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.

RA "A prolactin-releasing peptide in the brain." Nature 393:272-276 (1998).

RT -!- FUNCTION: STIMULATES PROLACTIN (PRL) RELEASE AND REGULATES THE EXPRESSION OF PROLACTIN THROUGH ITS RECEPTOR HGR3. MAY STIMULATE LACTOTROPHS DIRECTLY TO SECRETE PRL.

CC -!- TISSUE SPECIFICITY: MEULLA OBLONGATA AND HYPOTHALAMUS.

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CC DR EMBL: AB015417; BAA29025.1; -.

CC KW Hormone; Amidation; Signal; Cleavage on pair of basic residues.

CC FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.

FT PEPTIDE 33 53 PROLACTIN-RELEASING PEPTIDE PRRP20.

FT MOD_RES 53 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).

SQ SEQUENCE 98 AA; 10544 MW; 08AC35A13B0FA908 CRC64;

CC CC Query Match 92.9% Score 105; DB 1; Length 83; Best Local Similarity 90.0%; Pred. No. 7.8e-10; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC QY 1 TPDDINPAWASRGIRPVGRF 20

CC DB 33 TPDDINPAWYTSGIRPVGRF 52

RESULT 4

EXTL_HUMAN STANDARD; PRT; 676 AA.

ID EXTL_HUMAN

AC Q92935;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE EXOSTOSIN-LIKE 1 (EXOSTOSIN-L) (MULTIPLE EXOSTOSIS-LIKE PROTEIN). EXTL1 OR EXTL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TAXID=9606;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=97189339; PubMed=9037597;

RT "Identification and localization of the gene for EXTL, a third member of the multiple exostoses gene family." Genome Res. 7:10-16(1997).

RL [2] SEQUENCE FROM N.A.

RA Xu L., Deng H.X., Xia J.H., Pan Q., Liu C.Y.; "Mutations of the EXT genes in hereditary multiple exostoses in Chinese." Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

RN [3] SEQUENCE FROM N.A.

RA Willys W., Spijker N., Van Roy N., De Pepe A., De Bouie K., Willemse P.J., Van Huij W., Versteeg R., Spelmann F.; "Refined physical mapping and genomic structure of the EXTL1 gene." Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM (BY SIMILARITY).

RN SEQUENCE FROM N.A.

RP RA Willys W., Spijker N., Van Roy N., De Pepe A., De Bouie K., Willemse P.J., Van Huij W., Versteeg R., Spelmann F.; "Refined physical mapping and genomic structure of the EXTL1 gene." Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM (BY SIMILARITY).

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DR EMBL; AB01181: BAA32742.1; - .

DR INCHIPIO; IPK000345; - .

DR PROSITE; PS00190; CYTOCHROME_C; 4.

KW Electron transport; Photosynthesis; Reaction center; Heme;

KW Membrane; Lipoprotein; Duplication; Signal;

KW SIGNAL 1 22 BY SIMILARITY.

FT CHAIN 23 383 PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT.

FT LIPID 23 23 N-ACYL DIGLYCERIDE (BY SIMILARITY).

FT BINDING 107 107 HEME 1 (COVALENT) (BY SIMILARITY).

FT BINDING 110 110 HEME 1 (COVALENT) (BY SIMILARITY).

FT METAL 111 111 IRON 1 (HEME AXIAL LIGAND)

FT BINDING 152 152 (BY SIMILARITY).

FT BINDING 155 155 HEME 2 (COVALENT) (BY SIMILARITY).

FT METAL 156 156 IRON 2 (HEME AXIAL LIGAND)

FT BINDING 247 247 (BY SIMILARITY).

FT BINDING 250 250 HEME 3 (COVALENT) (BY SIMILARITY).

FT METAL 251 251 HEME 3 (COVALENT) (BY SIMILARITY).

FT BINDING 307 307 IRON 3 (HEME AXIAL LIGAND) (BY SIMILARITY).

FT BINDING 310 310 HEME 4 (COVALENT) (BY SIMILARITY).

FT METAL 311 311 HEME 4 (COVALENT) (BY SIMILARITY).

FT SEQUENCE 383 AA; 41522 MW; 96CD91FF1B9AE7E CRC64;

Query Match Best Local Similarity 40.7%; Score 46; DB 1; Length 383; Matches 8; Conservative 3; Mismatches 8; Indexes 0; Gaps 0;

QY 1 TPDINPAWWSRGRPVGR 19

Db 263 TPORTTAWYAIRHVRDING 281

RESULT 6

YAAJ_ECOLI STANDARD; PRT; 476 AA.

AC P30143;

DT 01-JUL-1993 (Rel. 26, created)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE HYPOOTHETICAL S1.7 KDA PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8).

GN YAAJ.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE:92334977; PubMed=1630901;

RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Michibuchi K., Nakata A.,

RA Riley M., Collier-Vides J., Glaser J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mai B., Shao Y.;

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE:97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glaser J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RT *The complete genome sequence of *Escherichia coli* K-12.";
 RL
 SCIENCE 277:1453-1474 (1997).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE SODIUM-ALANINE SYMPORTER FAMILY
 CC (SAF). STRONG, TO H. INFLUENZAE NIQ183.
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 CC
 DR EMBL; D10483; ; NOT_ANNOTATED_CDS.
 DR EMBL; AEO00011; AAC73118.1; .
 DR EcoGene; EG1155; Yral.
 DR InterPro; IPR001463; .
 DR Pfam; PF01235; Na_nAla_nSymp; 1.
 DR PRINTS; PR00175; Na_nAla_nSymp; 1.
 DR PROSITE; PS00873; NA_ALAMINE_SYMP; 1.
 KW Hypothetical protein; Transmembrane; Inner membrane; Transport;
 KW Symport.
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 141 161 POTENTIAL.
 FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 207 227 POTENTIAL.
 FT TRANSMEM 233 253 POTENTIAL.
 FT TRANSMEM 300 320 POTENTIAL.
 FT TRANSMEM 351 371 POTENTIAL.
 FT TRANSMEM 391 411 POTENTIAL.
 FT TRANSMEM 414 434 POTENTIAL.
 SQ SEQUENCE 476 AA; 51662 MW; 2F6BB2E12E126E63 CRC64;
 Query Match 38.9%; Score 44; DB 1; Length 476;
 Best Local Similarity 44.4%; Pred. No. 15;
 Matches 8; Conservative 3; Mismatches 1; Indels 6; Gaps 1;
 QY 3 DIN-----PAWYASRG1 14
 DB 120 DVMGQPRGGPAWYAMRL 137
 RESULT 7
 ARP_YEAST STANDARD; PRT; 719 AA.
 ID ARP YEAST STANDARD; PRT; 719 AA.
 AC P32770; Q12228; DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ARP PROTEIN.
 GN ARP1 OR ARP OR YDL167C.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC
 OC Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NCBI_TAXID=4932;
 RN [1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC STRAIN=AN22;
 RX MEDLINE-93247548; PubMed=8483449;
 RA Wehner E.P., Rao E., Brandel M.;
 RT "Molecular structure and genetic regulation of SPA, a gene
 responsible for resistance to formaldehyde in *Saccharomyces*
 RT cerevisiae, and characterization of its protein product.";
 RL Mol. Gen. Genet. 237:351-358 (1993).
 RN [2] SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Pohl T.M.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DDJB databases.

CC -!- SIMILARITY: CONTAINS 2 RANBP-TYPE ZINC FINGERS.
 CC -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
 CC
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 CC
 DR EMBL; X68020; CAA48159.1; .
 DR EMBL; 267750; CAA91579.1; .
 DR SGD; S274215; CAA98741.1; .
 DR InterPro; IPR000504; .
 DR InterPro; IPR001876; .
 DR Pfam; PF00076; Rrm; 1.
 DR Pfam; PF00641; zf-RanBP; 2.
 DR PROSITE; PS0102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
 KW Nuclear protein; zinc-finger; RNA-binding; Repeat;
 FT DOMAIN 226 322 RNA-BINDING (RRM).
 FT DOMAIN 490 564 ASN-RICK.
 FT CONFFLICT 493 493 I -> N (IM REF. 1).
 SQ SEQUENCE 719 AA; 79299 MW; ADA9BC09FD582669 CRC64;
 Query Match 38.9%; Score 44; DB 1; Length 719;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 7 AWYASRGIRPWG 18
 DB 244 SMFTQYGVRPVG 255
 RESULT 8
 VG12_BPP03 STANDARD; PRT; 860 AA.
 ID VG12_BPP03 STANDARD; PRT; 860 AA.
 AC Q37893; DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PRE-NECK APPENDAGE PROTEIN (LATE PROTEIN GP12).
 GN
 OS Bacteriophage B103.
 OC VIRUSES; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
 OC NEBI_TAXID=10776;
 RN {1} SEQUENCE FROM N.A.
 RP
 RX MEDLINE-98019084; PubMed=9358052;
 RA Pececn kova T., Benes V., Paces J., Vicek C., Paces V.;
 RT "Bacteriophage B103: complete DNA sequence of its genome and
 relationship to other *Bacillus* phages.";
 RL Gene 199:157-163 (1997).
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 CC
 DR EMBL; X99260; CAA67660.1; .
 DR Late protein; 860 AA; 91741 MW; AC5B38F4BC65ECB0 CRC64;
 SQ SEQUENCE 860 AA; 91741 MW; AC5B38F4BC65ECB0 CRC64;

Query Match

38.5%; Score 43.5; DB 1; Length 860;

DR PROSITE: PS00238: OPSIN; 1.
 KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; vision;
 KW Phosphorylation; G-protein coupled receptor.
 FT DOMAIN 1 46
 FT TRANSMEM 47 71
 DOMAIN 72 83
 FT TRANSMEM 84 108
 DOMAIN 109 123
 FT TRANSMEM 124 143
 DOMAIN 144 162
 FT TRANSMEM 163 186
 DOMAIN 187 210
 FT TRANSMEM 211 238
 DOMAIN 239 274
 FT TRANSMEM 275 298
 DOMAIN 299 306
 FT TRANSMEM 307 331
 DOMAIN 332 376
 FT DISULFID 376 397
 BINDING 318 318
 CARBOHYD 193 193
 SEQUENCE 376 AA; 42111 MW; FA964TC40531CBFB CRC64;

Query Match 38.1%; Score 43; DB 1; Length 376;
 Best Local Similarity 46.2%; Pred. No. 1B; Mismatches 3; Indels 0; Gaps 0;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 PDNPWASRGI 14
 | : | : | : | : |
 Db 40 PPMNPLWYSILGV 52

RESULT 11

LYTB MYCIE STANDARD; PRT; 332 AA.

ID LYTB_MYCIE
 AC 09X81;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LYTB PROTEIN HOMOLOG.
 GN LYTB OR MCB122.06C.
 OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae; Mycobacterium.
 OX NCBI_TAXID=1769;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Simmonds M.N.; Badcock K., James K.D., Parkhill J., Barrell B.G.,
 RA Rajandream M.A.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE LYTB FAMILY.

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CC DR EMBL; AE000144; AAC73481.1; -
 DR EMBL; U73857; ARB18101.1; -
 DR Ecogenie; EG1360; YairW.
 KW Hypothetical protein; YairW.
 SQ SEQUENCE 364 AA; 40414 MW; 7170FAF05C4E5973 CRC64;

Query Match 37.2%; Score 42; DB 1; Length 354;
 Best Local Similarity 56.2%; Pred. No. 23; Mismatches 9; Conservative 2; Mismatches 3; Indels 2; Gaps 1; Matches 7; Indels 0; Gaps 0;

QY 3 DINPWAWSRGIRKPGV 18
 | : | : | : | : | : |
 Db 270 DIDPAWLA--GVTIVG 283

RESULT 12

YAIR_ECOLI STANDARD; PRT; 364 AA.

ID YAIR_ECOLI
 AC P77562;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE NIPOHETICAL 40.4 KDA PROTEIN IN SBMA-DDLA INTERGENIC REGION.

GN YAIR.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RK MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mai B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
 RA Federici M., Hyman R., Kalman S., Koml O., Lew H., Lin D.,
 RA Namatin A., Oefner P., Roberts D., Schramm S., Davis R.W.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

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CC DR EMBL; AE000144; AAC73481.1; -
 DR EMBL; U73857; ARB18101.1; -
 DR Ecogenie; EG1360; YairW.
 KW Hypothetical protein; YairW.
 SQ SEQUENCE 364 AA; 40414 MW; 7170FAF05C4E5973 CRC64;

Query Match 37.2%; Score 42; DB 1; Length 354;
 Best Local Similarity 70.0%; Pred. No. 25; Mismatches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 DTNPWASR 12
 | : | : | : |
 Db 233 DENAGWASR 242

RESULT 13

CHOD_SRSQ STANDARD; PRT; 546 AA.

ID CHOD_SRSQ
 AC P12576;
 DT 01-OCT-1999 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-1989 (Rel. 12, Last annotation update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CHOLESTEROL OXIDASE PRECURSOR (EC 1.1.3.6) (CHOD).

GN CHOA.
 OS Streptomyces sp. (strain SA-COO).
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1931;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=B9113081; PubMed=2914858;
 RA Ishizaki T., Hiyama N., Shinkawa H., Nimi O., Murooka Y.;

Tue Apr 17 15:46:21 2001

us-09-446-543a-64.rsp

Page 8

DR Pfam; PF0065; rve; 1.
KW Transferase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
KW Endonuclease; Polypeptidase.
FT 1
SQ 843 AA; 9411 MW; 274C97731EE16C6A CRC64;

Query Match 37.2%; Score 42; DB 1; Length 843;
Best Local Similarity 41.2%; Pred. No. 59;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
Qy 1 TPDINPAWASRGKPV 17
|| | | :| |
Db 818 TPPKPSWRVQRSGNPL 834

Search completed: April 17, 2001, 15:48:52
Job time: 540 sec

GenCore version 4.5
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run on: April 17, 2001, 15:39:48 ; Search time 61.54 Seconds
(without alignments)
6.243 Million cell updates/sec

protein - protein search, using sw model

title: US-09-446-543R-64
perfect score: 113
sequence: BILOSUM62
scoring table: Gapop 10.0 , gapext 0.5
searched: 185757 seqs, 19210857 residues

total number of hits satisfying chosen parameters: 185757

minimum DB seq length: 0
maximum DB seq length: 200000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_AA:*

1: /ccgn2_6/ptodata/2/iaa/5A_COMB_pep:*

2: /ccgn2_6/ptodata/2/iaa/6A_COMB_pep:*

3: /ccgn2_6/ptodata/2/iaa/6B_COMB_pep:*

4: /ccgn2_6/ptodata/2/iaa/pcitus_COMB_pep:*

5: /ccgn2_6/ptodata/2/iaa/backfile1.pep:*

6: /ccgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	113	100.0	20	3	US-09-105-678A-46
2	113	100.0	21	3	US-09-105-678A-47
3	113	100.0	22	3	US-09-105-678A-48
4	113	100.0	31	3	US-09-105-678A-9
5	113	100.0	31	3	US-09-105-678A-43
6	113	100.0	32	3	US-09-105-678A-44
7	113	100.0	33	3	US-09-105-678A-45
8	109	96.5	20	3	US-09-105-678A-34
9	109	96.5	21	3	US-09-105-678A-35
10	109	96.5	22	3	US-09-105-678A-36
11	109	96.5	31	3	US-09-105-678A-7
12	109	96.5	31	3	US-09-105-678A-31
13	109	96.5	32	3	US-09-105-678A-32
14	109	96.5	33	3	US-09-105-678A-33
15	105	92.9	20	3	US-09-105-678A-40
16	105	92.9	21	3	US-09-105-678A-28
17	105	92.9	21	3	US-09-105-678A-41
18	105	92.9	22	3	US-09-105-678A-42
19	105	92.9	31	3	US-09-105-678A-8
20	105	92.9	31	3	US-09-105-678A-37
21	105	92.9	31	4	US-09-172-353-4
22	105	92.9	32	3	US-09-105-678A-38
23	105	92.9	33	3	US-09-105-678A-39
24	103	91.2	19	3	US-09-105-678A-30
25	98	86.7	29	3	US-09-105-678A-29
26	44	38.9	349	1	US-08-118-270-71
27	44	38.9	349	5	US-09-105-678A-45

ALIGNMENTS

RESULT	SEQUENCE	OPERATING SYSTEM	SOFTWARE	GENERAL INFORMATION
1	US-09-105-678A-46	1	Sequence 46, Application US/09105678A	Patent No. 610382
				APPLICANT: Suemaga, Masato
				APPLICANT: Moriya, Takeo
				APPLICANT: Tanaka, Yoko
				APPLICANT: Nishimura, Osamu
				APPLICATION NUMBER: US/09/105,678A
				CURRENT APPLICATION DATA:
				FILING DATE: 26-JUN-1998
				PRIOR APPLICATION DATA:
				APPLICATION NUMBER: JP 172118/1997
				FILING DATE: 27-JUN-1997
				ATTORNEY/AGENT INFORMATION:
				NAME: Collin, David G.
				REGISTRATION NUMBER: 27,026
				REFERENCE/DOCKET NUMBER: 48466-342
				TELECOMMUNICATION INFORMATION:
				TELEPHONE: 617-523-3400
				TELEFAX: 617-523-6440
				INFORMATION FOR SEQ ID NO: 46:
				SEQUENCE CHARACTERISTICS:
				LENGTH: 20 amino acids
				TYPE: amino acid
				STRANDEDNESS:
				TOPOLOGY: Linear
				MOLECULE TYPE: Peptide
				US-09-105-678A-45

Query Match Score 113; DB 3; Length 20;
Best Local Similarity 100.0%; Pct. No. 1e-11; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 QY 1 TPDINPAWYASRGIRPVGRF 20
 ; Sequence 47, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ; APPLICANT: Suenaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/105,678A
 ; FILING DATE: 26-JUN-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 172118/1997
 ; FILING DATE: 27-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conlin, David G.
 ; REGISTRATION NUMBER: 27,026
 ; REFERENCE/DOCKET NUMBER: 48466-342
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; INFORMATION FOR SEQ ID NO: 48:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 22 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 ; US-09-105-678A-48
 ;
 PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 172118/1997
 ; FILING DATE: 27-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conlin, David G.
 ; REGISTRATION NUMBER: 27,026
 ; REFERENCE/DOCKET NUMBER: 48466-342
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; INFORMATION FOR SEQ ID NO: 47:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-105-678A-47
 ;
 RESULT 3
 Query Match 100.0%; Score 113; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 20; conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPDINPAWYASRGIRPVGRF 20
 ; Sequence 48, Application US/09105678A
 ; Patent No. 6103882
 ; GENERAL INFORMATION:
 ; APPLICANT: Sueenaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/105,678A
 ; FILING DATE: 26-JUN-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 172118/1997
 ; FILING DATE: 27-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

RESULT 5
 US-09-105-678A-43
 Sequence 43, Application US/09105678A
 ; Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Sueuaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-105,678A.
 FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 6
 US-09-105-678A-44
 Sequence 44, Application US/09105678A
 ; Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Sueuaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-105,678A.
 FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 7
 US-09-105-678A-45
 Sequence 45, Application US/09105678A
 ; Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Sueuaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

Query Match 100.0%; Score 113; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.7e-11;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Query Match 100.0%; Score 113; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.7e-11;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 26-JUN-1998

PRIOR ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-09-105-678A-34

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-09-105-678A-45

Query Match 100.0%; Score 113; DB 3; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.8e-11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPDINPAWASRGIRPVGRF 20

Db 12 TPDINPAWASRGIRPVGRF 31

RESULT 8

US-09-105-678A-34

; Sequence 34: Application US/09105678A

; Patient No. 610382

; GENERAL INFORMATION:

; APPLICANT: Sueyaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Tanaka, Yoko

; TITLE OF INVENTION: METHOD OF PRODUCING A 19F2 LIGAND

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

PRIOR ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-09-105-678A-35

Query Match 96.5%; Score 109; DB 3; Length 21;

Best Local Similarity 95.0%; Pred. No. 4.6e-11;

Matches	19;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	TPDINPAWYASRGIRPGRF	20						
Db	1	TPDINPAWYAGRGIRPGRF	20						

RESULT 10
US-09-105-678A-36
; Sequence 36, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Suenaga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,678A
; FILING DATE: 26-JUN-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 48466-342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; FAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-105-678A-7

ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
FAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-105-678A-7

Query Match	95.5%	Score	109;	DB	3;	Length	31:
Best Local Similarity	95.0%;	Pred.	No.	4.9e-11;			
Matches	19;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
Qy	I	TPDINPAWYASRGIRPGRF	20				
Db	1	TPDINPAWYAGRGIRPGRF	20				

RESULT 11
US-09-105-678A-7
; Sequence 7, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Suenaga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,678A
; FILING DATE: 26-JUN-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: linear

MOLECULE TYPE: peptide

US-09-105-678A-31

Query Match

Best Local Similarity 95.0%; Pred. No. 7.4e-11; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 1;

RESULT 13 US-09-105-678A-32

Sequence 32, Application US/09105678A

GENERAL INFORMATION:

PATENT NO. 6103882

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESS: DKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: linear

MOLECULE TYPE: peptide

US-09-105-678A-33

RESULT 14 US-09-105-678A-33

Sequence 33, Application US/09105678A

GENERAL INFORMATION:

PATENT NO. 6103882

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESS: DKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: linear

MOLECULE TYPE: peptide

US-09-105-678A-31

RESULT 15 US-09-105-678A-40

Sequence 40, Application US/09105678A

GENERAL INFORMATION:

PATENT NO. 6103882

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48166-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLogy: Linear

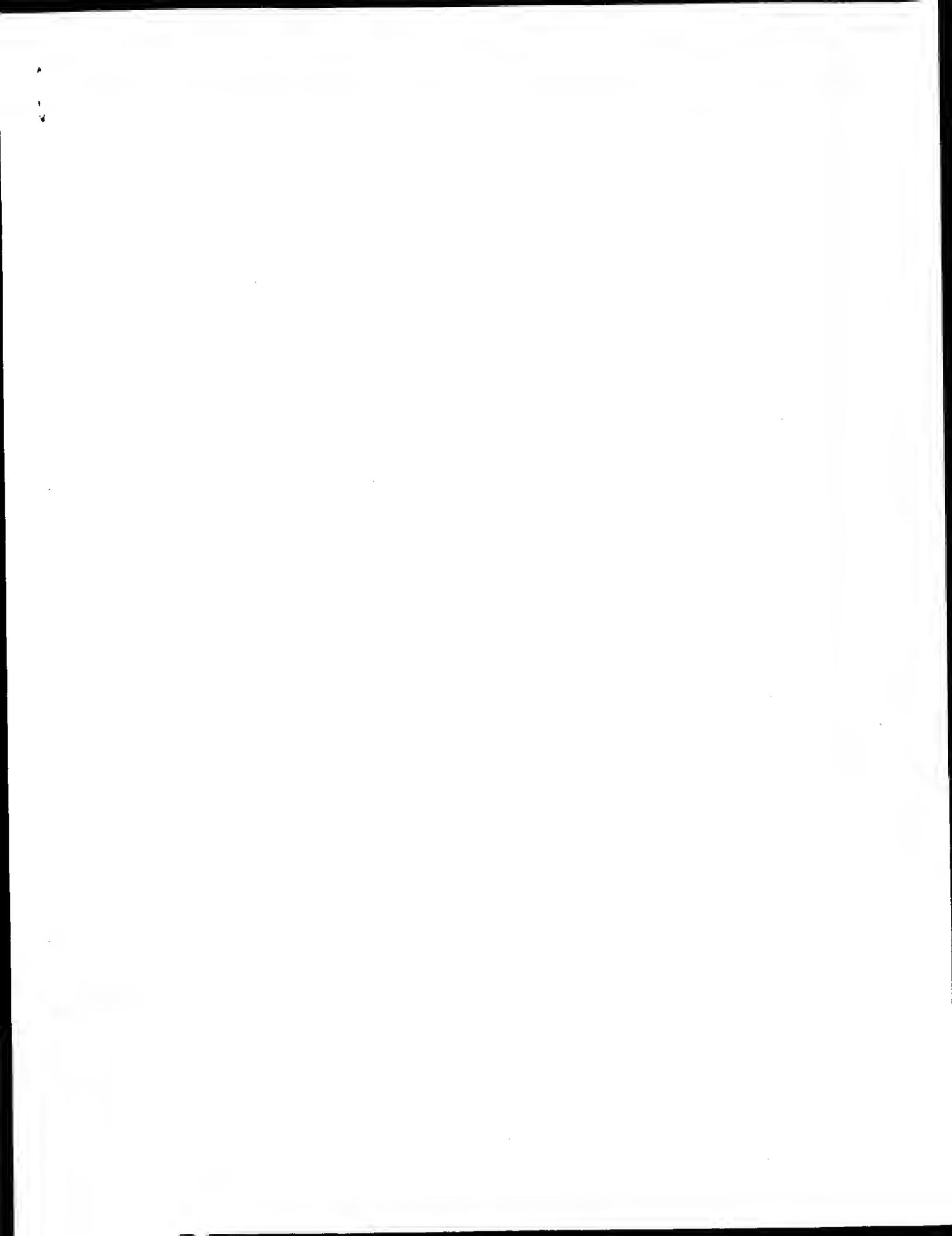
MOLECULE TYPE: peptide

US-09-105-678A-40

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Best Local Similarity 90.0%; Pred. No. 1.9e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	1	TPDINPAWYASRGIRPVGRF	20

Search completed: April 17, 2001, 15:39:48
Job time: 317 sec



GenCore version 4.5
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Human oxytocin secretagogue
19P2 ligand peptide
Human type G protein

OM protein - protein search, using sw model
Run on: April 17, 2001, 15:38:42 ; Search time 116.94 seconds
autocat="1100"

9.111 Million cell updates/sec
title: US-09-446-543A-64
perfect score: 113
sequence: 1 TPDINPAWYASRGIRPVGRF 20
scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext: 0.5
Total number of hits satisfying chosen parameters: 390729
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Match 100%

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ALIGNMENTS

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT	1	ALIGNMENTS
W31394		
ID	W31394 standard; Peptide; 20 AA.	
XX		
AC	W31394;	
XX		
DT	06-APR-1998 {first entry}	
XX		
DE	Human type G protein-coupled receptor ligand fragment 4.	
XX		
KW	G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9724436-A2.	
XX		
PD	10-JUL-1997.	
XX		
PF	26-DEC-1996; 96W0-JP03821.	
PR	18-SEP-1996; 96JP-0246573.	
PR	28-DEC-1995; 95JP-0343371.	
PR	12-MAR-1996; 96JP-0059419.	
PR	12-AUG-1996; 96JP-0211805.	
PA	(TAKA) TAKEDA CHEM IND LTD.	
XX		
PT	Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;	
PT	Kawamata Y, Kitada C;	
XX		
WP1;	1997-363672/33.	
DR	N-PSDB; V02431.	

XX
PT Ligand peptide for G protein-coupled receptor - acts by modulating
PT function in the central nervous system, pancreas and pituitary gland
XX
PS Claim 2; Page 185; 258pp; English.

XX
CC This sequence represents a peptide fragment from a novel human type
CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the
CC sequence represented in W31190 and is used in an assay to monitor ligand
CC binding to the G protein-coupled receptor protein. Pharmaceutical
CC compositions containing this ligand may be used as a pituitary function
CC modulator, a central nervous system modulator or a pancreatic function
CC modulator. This ligand could have specific applications as a prophylactic
CC or therapeutic agent for dementia, depression, hyperkinetic syndrome,
CC disturbance of consciousness, anxiety syndrome, Schizophrenia, trauma,
CC growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia,
CC hypercholesterolaemia, hyperglyceraidaemia, diabetes,
CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma,
CC rheumatoid arthritis, spinal injury, transient brain Ischaemia, epilepsy,
CC amyotrophic lateral sclerosis, acute myocardial infarction, infertility,
CC spinocerebellar degeneration, bone fracture, trauma, topical dermatitis,
CC osteoporosis and/or oligogalactia. Assays can also be developed to screen
CC compounds which are capable of altering the binding activity of the
XX ligand affecting activation of the G protein coupled receptor protein.
SQ Sequence 20 AA:

Query Match 100.0%; Score 113; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPDINPAWYASRGIRPVGRF 20
Db 1 tpdinpawyasrgirpvgrf 20

RESULT 2
W97236 ID W97236 standard; peptide: 20 AA.

XX AC W97236;
XX DT 06-MAY-1999 (first entry)
XX DE Human type ligand polypeptide fragment.
XX KW Rat type ligand; modulation; prolactin secretion;
XX G protein-coupled receptor; GPCR; hypocoarvarianism; gonocyst cacogenesis;
XX menopausal syndrome; euthyroid; hypometabolism; lactation;
XX pituitary adenomas; brain tumour; emmenopatly; autoimmune disease;
XX prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
XX acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome;
XX Forbes-Albright syndrome; lymphoma; Sheehan syndrome;
XX Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dysospermia;
XX contraceptive; placental function; choriocarcinoma; hydatid mole;
XX irruption mole; abortion; unthrifly fetus; abnormal saccharometabolism;
XX abnormal lipidmetabolism; oxytocia.
OS Homo sapiens.
XX PN WO9858962-A1.

XX PR 23-JUN-1997; 97JP-0165437.
XX PD 30-DEC-1998.
XX PF 22-JUN-1998; 98WO-JP02765.

XX PR (TAKE) TAKEDA CHEM IND LTD.
XX PT Fujii R, Hinuma S, Kawamata Y, Matsumoto H;
XX DR WPI; 1999-105614/09.

XX
PT Use of G protein-coupled receptor ligands - for modulating prolactin
PT secretion or placental function, e.g. for treating menopausal
PT syndrome, tumours, autoimmune disease or abnormal pregnancy
XX
PS Claim 3; Page 166; 241pp; English.

XX
CC The present sequence represents a human type ligand fragment. It
CC is used in the course of the invention. The specification describes
CC an agent for modulating Prolactin secretion which comprises a
CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
CC protein. The agents for promoting prolactin secretion can be used for
CC treating or preventing hypopituitarism, gynaest cacogenesis, menopausal
CC syndrome, euthyroid or hypometabolism. They can be used for promoting
CC lactation in a domestic mammal and as an aphrodisiac. The agents for
CC inhibiting prolactin secretion can be used for treating or preventing
CC pituitary adenomatosis, brain tumour, emmenopatly, autoimmune disease,
CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome,
CC Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dysospermia.
CC The inhibitory agents can also be used as contraceptives. The agents for
CC modulating Placental function also can be used for treating or preventing
CC choriocarcinoma, hydatid mole, abortion, unthrifly fetus,
CC abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
XX
SQ Sequence 20 AA:

Query Match 100.0%; Score 113; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPDINPAWYASRGIRPVGRF 20
Db 1 tpdinpawyasrgirpvgrf 20

RESULT 3
B10365 ID B10365 standard; peptide: 20 AA.

XX AC B10365;
XX DT 24-NOV-2000 (first entry)
XX DE Human oxytocin secretion Promoting Peptide SEQ ID NO: 35.

XX KW Human; oxytocin secretion promoter; G protein-coupled receptor protein;
XX treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
XX cesarean section; artificial fertilization; galactostasis; goat; pig;
XX veterinary medicine; milk production.
XX OS Homo sapiens.
XX PN WO200038704-A1.

XX PD 06-JUL-2000.
XX PF 22-DEC-1999; 99WO-JP07199.
XX PR 25-DEC-1998; 99JP-0369565.

XX PA (TAKE) TAKEDA CHEM IND LTD.
XX PT Matsumoto H, Kitada C, Hinuma S;
XX DR WPI; 2000-452299-39.
XX
PT Physiologically-active polypeptide recognized as ligand by G
PT protein-coupled receptor protein, for promoting secretion of oxytocin,
PT as drugs for diseases relating to oxytocin secretion and in veterinary
PT medicine -

PS Disclosure; Page 63; 72pp; Japanese.

XX
CC This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g., weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion promoter.

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 113; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPDINPAWASRGIRGVGRF 20
Db 1 tpdinpawasrgirgvgrf 20

RESULT 4

Y49294 ID Y49294 standard; peptide; 20 AA.

AC Y49294;

XX DT 22-FEB-2000 (first entry)

XX DE 19P2 ligand peptide fragment.

XX KW Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic. OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Modified-site 20
ET /note= "C-terminal amide"

XX PN WO9960112-A1.

XX PD 25-NOV-1999.

XX PR 20-MAY-1999; 99WO-JP02650.

XX PR 21-MAY-1998; 98JP-010293.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PT Matsumoto H, Kitada C, Hinuma S;

XX DR WPI; 2000-039381/03.

XX PT New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality

XX PS disclosure; Page 26; 73pp; Japanese.

The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences Y49290-302 represent peptide fragments of the 19P2 ligand.

SQ Sequence 20 AA;

Query Match 100.0%; Score 113; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPDINPAWASRGIRGVGRF 20
Db 1 tpdinpawasrgirgvgrf 20

RESULT 5

W31395 ID W31395 standard; Peptide; 21 AA.

AC W31395;

DT 05-APR-1998 (first entry)

XX Human type G protein-coupled receptor ligand fragment 5.
DE G protein-coupled receptor; ligand binding; pharmaceutical; KW modulator; pituitary; central nervous system; pancreas; prophylactic; KW therapeutic agent.

XX OS Homo sapiens.

XX PN WO9724436-A2.

XX PD 10-JUL-1997.

XX PF 26-DEC-1996; 96WO-JP03821.

XX PR 18-SEP-1996; 96JP-0246573.

PR 28-DEC-1995; 95JP-02443371.

PR 15-MAR-1996; 96JP-0059419.

PR 12-AUG-1996; 96UP-0211805.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PT Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;

XX PI Kawamata Y, Kitada C;

XX DR WPI; 1997-363672/33.

XX DR N-PSDB; v02432.

XX PT Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland

XX PS Claim 2; Page 186; 258pp; English.

XX CC This sequence represents a peptide fragment from a novel human type

CC ligand polypeptide corresponding to amino acid residues 34 to 54 of the sequence represented in W31390 and is used in an assay to monitor ligand binding to the G protein coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretery disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolemia, hyperglyceraidemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amyotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.

SQ Sequence 21 AA;

Query Match 100.0%; Score 113; DB 18; Length 21; ID W31396 standard; peptide; 22 AA.
 Best Local Similarity 100.0%; Pred. No. 3.7e-12; AC W31396;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX
 QY 1 TPDINPAWYASRGIRPVGRF 20
 Db 1 tpdinpawyasrgirpvgrf 20

RESULT 6 ID B10366 standard; peptide; 21 AA.
 XX
 AC B10366;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Human oxytocin secretion promoting peptide SEQ ID NO: 36.
 XX
 KW Human; oxytocin secretion promoter; G protein-coupled receptor protein;
 KW treatment; disease; pain; tonic bleeding; uterine recovery failure; cow;
 KW caesarean section; artificial fertilization; galactostasis; goat; pig;
 KW veterinary medicine; milk production.
 XX
 OS Homo sapiens.
 XX
 PN WO20008704-A1.
 XX
 PD 06-JUL-2000.
 XX
 PF 22-DEC-1999; 99WO-JP07199.
 XX
 PR 25-DEC-1998; 98JP-0369585.
 XX
 PA (TKE) TAKEDA CHEM IND LTD.
 XX
 PT Matsumoto H, Kitada C, Hinuma S;
 XX
 DR WPI: 2000-452298/39.
 XX
 PT Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine
 XX
 PS Disclosure; Page 63; 72PP; Japanese.
 XX
 CC This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g., weak pains and atomic bleeding, before and after expulsion of Placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion promoter.
 XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 113; DB 21; Length 21; ID W31396 standard; peptide; 22 AA.
 Best Local Similarity 100.0%; Pred. No. 3.9e-12; AC W31396;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX
 QY 1 TPDINPAWYASRGIRPVGRF 20
 Db 1 tpdinpawyasrgirpvgrf 20

RESULT 8 ID B10367 standard; peptide; 22 AA.
 XX
 W31396 XX

AC AC
XX B10367;
DT XX
XX 24-NOV-2000 (first entry)
DE Human oxytocin secretion promoting peptide SEQ ID NO: 37.
XX KW Human; oxytocin secretion promoter; G protein-coupled receptor protein;
KW treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
KW caesarean section; artificial fertilization; galactostasis; goat; pig;
KW veterinary medicine; milk production.
OS OS
Homo sapiens.
XX PN WO200038704-A1.
PN XX
PD 06-JUL-2000.
XX PF 22-DEC-1999; 99WO-JP07199.
PR 25-DEC-1998; 98JP-0369585.
PA {TAKE } TAKEDA CHEM IND LTD.
XX PI Matsumoto H, Kitada C, Hinuma S;
XX DR WPI; 2000-452298/39.
XX PS Disclosure; Page 64; 72PP; Japanese.

PT Physiologically active polypeptide recognized as ligand by G protein-coupled receptor Protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine

PT Disclosure; Page 64; 72PP; Japanese.

CC This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g., weak pains and atomic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion promoter.

CC Sequence 22 AA;

SO Query Match 100.0%; Score 113; DB 21; Length 22;
Best Local Similarity 100.0%; Score 113; DB 21; Length 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPDINPAWYASRGIRPVGRF 20
Db 1 tpdinpawyasrgirpvgrf 20

RESULT 9
W31391 Human type G protein-coupled receptor ligand fragment 1.
ID W31391 standard; Peptide; 31 AA.
AC W31391;
XX DT 06-APR-1998 (first entry)
DE Human type G protein-coupled receptor ligand fragment 1.
XX KW G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.
XX OS Homo sapiens.

RESULT 10
W97235 Human type ligand polypeptide fragment.
ID W97235 standard; peptide; 31 AA.
AC W97235;
XX DT 06-MAY-1999 (first entry)
DE Human type ligand polypeptide fragment.
XX KW Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypoparathyroidism; gonocyst; cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; ameniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole;

KW
abnormal lipidmetabolism; oxytocia;
XX
OS Homo sapiens.
XX
PN WO958962-A1.
XX
PD 30-DEC-1998.
XX
PR 27-JUN-1997; 97JP-017211B.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Moriya T, Nishimura O, Suenaga M, tanaka Y;
XX
PF 22-JUN-1998; 98WO-JP02765.
XX
PR 23-JUN-1997; 97JP-0165437.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Fujii R, Hinuma S, Kawamata Y, Matsumoto H;
XX
PR 1999-047884/05.
XX
DR WPI; 1999-105614/03.
XX
PT Use of G protein-coupled receptor ligands - for modulating prolactin
secretion or placental function, e.g. for treating menopausal
syndrome, tumours, autoimmune disease or abnormal pregnancy
XX
PS Claim 3; Page 159; 24pp; English.
XX
CC The present sequence represents a human type ligand fragment. It
is used in the course of the invention. The specification describes
an agent for modulating prolactin secretion which comprises a
ligand polypeptide or a salt for a G protein-coupled receptor (GPCR)
protein. The agents for promoting prolactin secretion can be used for
treating or preventing hypopituitarism, gonocyst carcinoma, menopausal
syndrome, euthyroid or hypometabolism. They can be used for promoting
lactation in a domestic mammal and as an aphrodisiac. The agents for
inhibiting prolactin secretion can be used for treating or preventing
pituitary adenomatus, brain tumour, emmenopathy, autoimmune disease,
prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome,
Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
CC The inhibitory agents can also be used as contraceptives. The agents for
modulating placental function can be used for treating or preventing
choriocarcinoma, hydatid mole, abortion, unthrifly fetus,
abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 113; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.BE-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TPPDINPAWYASRGIRPVGRF 20
Db 12 tpdinpawyasrgirpvgrf 31

RESULT 11
W87615
ID W87615 standard; Peptide; 31 AA.
XX
AC W87615;
XX
DT 29-MAR-1999 (first entry)
XX
DE Human 19P2 ligand.
XX
KW 19P2 ligand; G protein coupled receptor; pituitary;
KW prolactin releasing peptide; human; dementia; breast cancer;
KW therapy.
XX
OS Homo sapiens.
XX
PN EP887417-A2.

Query Match 100.0%; Score 113; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.BE-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TPPDINPAWYASRGIRPVGRF 20
Db 12 tpdinpawyasrgirpvgrf 31

RESULT 12
B10362
ID B10362 standard; Peptide; 31 AA.
XX
AC B10362;
XX
DT 24-NOV-2000 (first entry)
XX
DE Human oxytocin secretion promoting Peptide SEQ ID NO: 32.
XX
Human; oxytocin secretion promoter; G protein-coupled receptor protein;
KW treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
KW caesarean section; artificial fertilization; galactostasis; goat; pig;
KW veterinary medicine; milk production.

XX
OS Homo sapiens.
XX
PN WO20038704-A1.
XX
PD 06-JUL-2000.
XX
PF 22-DEC-1999; 99WO-JP07199.
XX
PR 25-DEC-1998; 98JP-0369585.
XX
PA {TAKE } TAKEDA CHEM IND LTD.
XX
PI Matsumoto H, Kitada C, Hinuma S;
DR WPI; 2000-039381/03.
XX
PT New monoclonal antibodies, useful in diagnosis, as drugs and in
studying diseases related to ligand abnormality -
XX
PS Disclosure; Page 26; 73PP; Japanese.
XX
CC This invention describes a novel oxytocin secretion-regulating agent
which contains a ligand peptide or its salt for the G protein-coupled
receptor protein. It is useful in the form of drugs for ameliorating,
preventing and treating diseases relating to oxytocin secretion e.g.,
weak pains and atomic bleeding, before and after expulsion of placenta,
uterine recovery failure, cesarean section, stoppage of artificial
fertilization or galactostasis and is also applicable in veterinary
medicine for promoting milk production in cow, goat and pig. This
sequence represents a human peptide which acts as an oxytocin secretion
XX
CC promoter.
XX
PS Disclosure; Page 62; 72pp; Japanese.
SQ Sequence 31 AA:
Query Match 100.0%; Score 113; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC Y49291; Y49291;
DB 12 tpdinpawyasrgirpvgrf 31

RESULT 13
Y49291
ID Y49291 standard; peptide; 31 AA.
XX
AC Y49291;
XX
DT 22-FEB-2000 (first entry)
XX
DE 19P2 ligand peptide fragment.
XX
KW Monoclonal antibody; 19P2 ligand; diagnosis; proactin secretion;
pituitary; regulatory mechanism; central nervous system; pancreatic.
XX
OS Homo sapiens.
XX
FH Key Modified-site Location/Qualifiers
FT 31 /note= "C-terminal amide"
XX
PN WO9360112-A1.
XX
PD 25-NOV-1999.
XX
PR 20-MAY-1999; 99WO-JP02650.
XX
PR 21-MAY-1998; 98JP-0140293.

SQ Sequence 31 AA:
Query Match 100.0%; Score 113; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC W31392; W31392;
XX
DT 06-APR-1998 (first entry)
XX
DE Human type G protein-coupled receptor ligand fragment 2.
XX
KW G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
XX
OS Homo sapiens.
XX
PN WO9724436-A2.
XX
PD 10-JUL-1997.
XX
PF 26-DEC-1996; 96WO-JP03821.
XX
PR 18-SEP-1996; 96JP-0246573.
PR 28-DEC-1995; 95JP-0343371.
PR 15-MAR-1996; 96JP-0059419.
PR 12-AUG-1996; 96JP-0211805.
XX
PA {TAKE } TAKEDA CHEM IND LTD.
XX
PI Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
PR Kawamata Y, Kitada C;
DR WPI; 1997-63672/33.
XX
N-PSDB; V02429.
XX
PT Ligand peptide for G Protein-coupled receptor - acts by modulating
function in the central nervous system, pancreas and pituitary gland
XX
PS Claim 2; Page 185; 258pp; English.

XX
 CC This sequence represents a peptide fragment from a novel human type
 CC ligand polypeptide corresponding to amino acid residues 23 to 54 of the
 CC sequence represented in W31390 and is used in an assay to monitor ligand
 CC binding to the G protein-coupled receptor protein. Pharmaceutical
 CC compositions containing this ligand may be used as a pituitary function
 CC modulator, a central nervous system modulator or a pancreatic function
 CC modulator. This ligand could have specific applications as a prophylactic
 CC or therapeutic agent for dementia, depression, hyperkinetic syndrome,
 CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
 CC growth hormone secretory disease, hyper- and polyphagia, hypoprolactinaemia,
 CC hypercholesterolaemia, hyperglycaemia, hyperlipidaemia,
 CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma,
 CC rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy,
 CC amyotrophic lateral sclerosis, acute myocardial infarction, infertility,
 CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
 CC osteoporosis and/or oligoagactia. Assays can also be developed to screen
 CC compounds which are capable of altering the binding activity of the
 XX ligand affecting activation of the G protein-coupled receptor protein.

SQ Sequence 32 AA:

Query Match 100.0%; Score 113; DB 18; Length 32;

Best Local Similarity 100.0%; Pred. No. 6.1e-12; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 TPPDINPAWYASRGIRPVGRF 20
 Db 12 tpdinpawasrgirpvgrf 31

Search completed: April 17, 2001, 15:38:42

Job time: 349 sec

CC preventing and treating diseases relating to oxytocin secretion e.g.
 CC weak pains and atonic bleeding, before and after expulsion of placenta,
 CC uterine recovery failure, caesarean section, stoppage of artificial
 CC fertilization or galactostasis and is also applicable in veterinary
 CC medicine for promoting milk production in cow, goat and pig. This
 CC sequence represents a human peptide which acts as an oxytocin secretion
 CC promoter.

SQ Sequence 32 AA:

Query Match 100.0%; Score 113; DB 21; Length 32;

Best Local Similarity 100.0%; Pred. No. 6.1e-12; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 TPPDINPAWYASRGIRPVGRF 20
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Query Match 100.0%; Score 113; DB 18; Length 32;

Best Local Similarity 100.0%; Pred. No. 6.1e-12; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Db 12 tpdinpawasrgirpvgrf 31

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Query Match 100.0%; Score 113; DB 18; Length 32;

Best Local Similarity 100.0%; Pred. No. 6.1e-12; Indels 0; Gaps 0;
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Query Match 100.0%; Score 113; DB 18; Length 32;

Best Local Similarity 100.0%; Pred. No. 6.1e-12; Indels 0;

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